
Release 2.1D John F. Collins, Biocomputing Research Unit.


MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Nov 17 08:30:37 1995; MasPar time 12.94 Seconds
585.410 Million cell updates/sec

Tabular output not generated.

Title: >US-08-380-051-2
Description: (1:494) from US08380051.pep
Perfect Score: 3614
Sequence: 1 MLKLIVPFLKRESAFNEMTM.....KTETDMSLHPLLQEIYKDLY 494

Scoring table: PAM 150
Gap 11

Searched: 43470 seqs, 15335248 residues

Database: swiss-prot31
1 part1
2 part2
3 part3
4 part4
5 part5
6 part6
7 part7
8 part8

Statistics: Mean 52.508; Variance 112.681; scale 0.466

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 3433 | 95.0 | 475 | 6 | PPAT_HUMAN | PEROXISOME PROLIFERAT | 0.00e+00 |
| 2 | 3311 | 91.6 | 470 | 6 | PPAT_MOUSE | PEROXISOME PROLIFERAT | 0.00e+00 |
| 3 | 2579 | 71.4 | 477 | 6 | PPAT_XENLA | PEROXISOME PROLIFERAT | 0.00e+00 |
| 4 | 1946 | 53.8 | 468 | 6 | PPAR_HUMAN | PEROXISOME PROLIFERAT | 0.00e+00 |
| 5 | 1932 | 53.5 | 468 | 6 | PPAR_MOUSE | PEROXISOME PROLIFERAT | 0.00e+00 |
| 6 | 1930 | 53.4 | 468 | 6 | PPAR_RAT | PEROXISOME PROLIFERAT | 0.00e+00 |
| 7 | 1921 | 53.2 | 441 | 6 | PPAS_HUMAN | PEROXISOME PROLIFERAT | 0.00e+00 |
| 8 | 1894 | 52.4 | 474 | 6 | PPAR_XENLA | PEROXISOME PROLIFERAT | 0.00e+00 |
| 9 | 1886 | 52.2 | 440 | 6 | PPAS_MOUSE | PEROXISOME PROLIFERAT | 0.00e+00 |
| 10 | 1743 | 48.2 | 396 | 6 | PPAS_XENLA | PEROXISOME PROLIFERAT | 1.37e-303 |



| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 11 | 706 | 19.5 | 1237 | 2 | E75A_DROME | ECDYSONE-INDUCIBLE PR | 6.45e-103 |
| 12 | 641 | 17.7 | 1443 | 2 | E75C_DROME | ECDYSONE-INDUCIBLE PR | 9.62e-91 |
| 13 | 558 | 15.4 | 158 | 6 | PPAU_MOUSE | PEROXISOME PROLIFERAT | 2.36e-75 |
| 14 | 528 | 14.6 | 1394 | 2 | E75B_DROME | ECDYSONE-INDUCIBLE PR | 7.64e-70 |
| 15 | 525 | 14.5 | 369 | 7 | THB1_XENLA | THYROID HORMONE RECEP | 2.71e-69 |
| 16 | 525 | 14.5 | 373 | 7 | THB5_XENLA | THYROID HORMONE RECEP | 2.71e-69 |
| 17 | 518 | 14.3 | 369 | 7 | THB_CHICK | THYROID HORMONE RECEP | 5.16e-68 |
| 18 | 518 | 14.3 | 476 | 7 | THB2_HUMAN | THYROID HORMONE RECEP | 5.16e-68 |
| 19 | 517 | 14.3 | 410 | 7 | THA1_MOUSE | THYROID HORMONE RECEP | 7.86e-68 |
| 20 | 516 | 14.3 | 410 | 7 | THA1_HUMAN | THYROID HORMONE RECEP | 1.20e-67 |
| 21 | 514 | 14.2 | 461 | 7 | THB1_MOUSE | THYROID HORMONE RECEP | 2.78e-67 |
| 22 | 514 | 14.2 | 475 | 7 | THB2_MOUSE | THYROID HORMONE RECEP | 2.78e-67 |
| 23 | 512 | 14.2 | 461 | 7 | THB1_HUMAN | THYROID HORMONE RECEP | 6.44e-67 |
| 24 | 511 | 14.1 | 373 | 7 | THB6_XENLA | THYROID HORMONE RECEP | 9.80e-67 |
| 25 | 511 | 14.1 | 414 | 7 | THB7_XENLA | THYROID HORMONE RECEP | 9.80e-67 |
| 26 | 510 | 14.1 | 461 | 7 | THB1_RAT | THYROID HORMONE RECEP | 1.49e-66 |
| 27 | 510 | 14.1 | 514 | 7 | THB2_RAT | THYROID HORMONE RECEP | 1.49e-66 |
| 28 | 510 | 14.1 | 410 | 7 | THA1_RAT | THYROID HORMONE RECEP | 1.49e-66 |
| 29 | 503 | 13.9 | 408 | 7 | THA_CHICK | THYROID HORMONE RECEP | 2.82e-65 |
| 30 | 495 | 13.7 | 418 | 7 | THA_RANCA | THYROID HORMONE RECEP | 8.07e-64 |
| 31 | 490 | 13.6 | 614 | 2 | EAR1_HUMAN | V-ERBA RELATED PROTEI | 6.54e-63 |
| 32 | 486 | 13.4 | 418 | 7 | THAA_XENLA | THYROID HORMONE RECEP | 3.48e-62 |
| 33 | 475 | 13.1 | 418 | 7 | THAB_XENLA | THYROID HORMONE RECEP | 3.43e-60 |
| 34 | 474 | 13.1 | 385 | 3 | ERBA_AVIER | ERBA ONCOGENE PROTEIN | 5.21e-60 |
| 35 | 465 | 12.9 | 455 | 6 | RRB1_CHICK | RETINOIC ACID RECEPTO | 2.21e-58 |
| 36 | 465 | 12.9 | 448 | 6 | RRB2_CHICK | RETINOIC ACID RECEPTO | 2.21e-58 |
| 37 | 464 | 12.8 | 462 | 6 | RRA1_HUMAN | RETINOIC ACID RECEPTO | 3.34e-58 |
| 38 | 463 | 12.8 | 462 | 6 | RRA1_MOUSE | RETINOIC ACID RECEPTO | 5.07e-58 |
| 39 | 463 | 12.8 | 459 | 6 | RRA2_MOUSE | RETINOIC ACID RECEPTO | 5.07e-58 |
| 40 | 462 | 12.8 | 458 | 6 | RRA_NOTVI | RETINOIC ACID RECEPTO | 7.68e-58 |
| 41 | 459 | 12.7 | 448 | 6 | RRB2_HUMAN | RETINOIC ACID RECEPTO | 2.67e-57 |
| 42 | 456 | 12.6 | 455 | 6 | RRB1_MOUSE | RETINOIC ACID RECEPTO | 9.27e-57 |
| 43 | 456 | 12.6 | 482 | 6 | RRB3_MOUSE | RETINOIC ACID RECEPTO | 9.27e-57 |
| 44 | 456 | 12.6 | 448 | 6 | RRB2_MOUSE | RETINOIC ACID RECEPTO | 9.27e-57 |
| 45 | 455 | 12.6 | 443 | 6 | RRG2_HUMAN | RETINOIC ACID RECEPTO | 1.40e-56 |

ALIGNMENTS

RESULT 1
ID PPAT_HUMAN STANDARD; PRT; 475 AA.
AC P37231;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA (PPAR-GAMMA).
GN PPARG.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA APERLO C., POGNONEC P., AUWERX J., BOULUKOS K.;
RL SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC NUCLEAR HORMONE RECEPTORS.

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DR   EMBL; Z30972; CGPPARRN.
DR   PIR; S42489; S42489.
DR   HSSP; P10826; 1HRA.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND     109    173       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      109    129       C4-TYPE.
FT   ZN_FING      146    168       C4-TYPE.
FT   DOMAIN       288    475       LIGAND-BINDING (POTENTIAL).
SQ   SEQUENCE   475 AA;  54472 MW;  1146250 CN;

  DB  6;  Score    3433;  Match 97.7%;  QryMatch 95.0%;  Pred. No. 0.00e+00;
  Matches   464;  Conservative   11;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 mvdtempfwptnfgissvdlsmmddhshsfdikpfttvdfssisaphyedipftradpmv 60
          ||||||||||||||||||||:|:|||||||||||||||||||:||||||||||:||:|
Qy     20 MVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDPVV 79

Db     61 adykydlklqeyqsaikvepasppyysekaqlynrpheepsnslmaiecrvcgdkasgfh 120
          ||||||||||||||||||||||||||||:||||:||||||||||||||||||||||||
Qy     80 ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGDKASGFH 139

Db    121 ygvhacegckgffrrtirlkliydrcdlncrihkksrnkcqycrfqkclavgmshnairf 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    140 YGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRF 199

Db    181 grmpqaekekllaeissdidqlnpesadlralakhlydsyiksfpltkakarailtgktt 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    200 GRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTT 259

Db    241 dkspfviydmnslmmgedkikfkhitplqeqskevairifqgcqfrsveavqeiteyakn 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Qy    260 DKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKS 319

Db    301 ipgfinldlndqvtllkygvheiiytmlaslmnkdgvliseqqgfmtreflkslrkpfgd 360
          ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    320 IPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGD 379

Db    361 fmepkfefavkfnalelddsdlaifiaviilsgdrpgllnvkpiediqdnllqalelqlk 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    380 FMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLK 439

Db    421 lnhpessqlfakvlqkmtdlrqivtehvqllhvikktetdmslhpllqeiykdly 475
          ||||||||||:||||||||||||||||:||||||||||||||||||||||||||||
Qy    440 LNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 494


RESULT    2
ID   PPAT_MOUSE     STANDARD;      PRT;   470 AA.
AC   P37238;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA (PPAR-GAMMA).
GN   PPARG.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=HEART;
RM   94059089
RA   CHEN F., LAW S.W., O'MALLEY B.W.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 196:671-677(1993).
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CC   -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC       HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC       THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC       OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC       PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
DR   EMBL; U01664; MM664.
DR   PIR; JN0881; JN0881.
DR   HSSP; P10826; 1HRA.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND     109    173       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      109    129       C4-TYPE.
FT   ZN_FING      146    168       C4-TYPE.
FT   DOMAIN       288    470       LIGAND-BINDING (POTENTIAL).
SQ   SEQUENCE   470 AA;  54014 MW;  1131104 CN;

  DB  6;  Score    3311;  Match 96.2%;  QryMatch 91.6%;  Pred. No. 0.00e+00;
  Matches   457;  Conservative   11;  Mismatches   2;  Indels   5;  Gaps   1;

Db      1 mvdtempfwptnfgissvdlsvmedhshsfdikpfttvdfssisaphyedipftradpmv 60
          ||||||||||||||||||||||||||||||||||||||||||:||||||||||:||:|
Qy     20 MVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDPVV 79

Db     61 adykydlklqeyqsaikvepasppyysektqlynrpheepsnslmaiecrvcgdkasgfh 120
          ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Qy     80 ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGDKASGFH 139

Db    121 ygvhacegckgffrrtirlkliydrcdlncrihkksrnkcqycrfqkclavgmshnairf 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    140 YGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRF 199

Db    181 grdrqaekekllaeissdidqlnpesadlralakhlydsyiksfpltkakarailtgktt 240
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    200 GRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTT 259

Db    241 dkspfviydmssfmmgedkikfkhitplqeqskevairifqgcqfrsveavqeiteyakn 300
          ||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||:
Qy    260 DKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKS 319

Db    301 ipgfinldlndqvtllkygvheiiytmlaslmnkdgvliseqqgfmtreflkslrkpfgd 360
          ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    320 IPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGD 379

Db    361 fmepkfefavkfnalelddsdlaifiaviilsgdrpgllnvkpiediqdnllq-----lk 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||      ||
Qy    380 FMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLK 439

Db    416 lnhpessqlfakvlqkmtdlrqivtehvqllhvikktetdmslhplfqeiykdly 470
          ||||||||||:|||||||||||||||:||||||||||||||:||||||||
Qy    440 LNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 494


RESULT    3
ID   PPAT_XENLA     STANDARD;      PRT;   477 AA.
AC   P37234;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-GAMMA).
GN   PPARG.
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OS   XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92191267
RA   DREYER C., KREY G., KELLER H., GIVEL F., HELFTENBEIN G., WAHLI W.;
RL   CELL 68:879-887(1992).
RN   [2]
RP   CHARACTERIZATION.
RM   94100165
RA   KREY G., KELLER H., MAHFOUDI A., MEDIN J., OZATO K., DREYER C.,
RA   WAHLI W.;
RL   J. STEROID BIOCHEM. MOL. BIOL. 47:65-73(1993).
CC   -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC       HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC       THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC       OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC       PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC   -!- TISSUE SPECIFICITY: EXPRESSED MAINLY IN ADIPOSE TISSUE AND KIDNEY.
CC   -!- DEVELOPMENTAL STAGE: ADULT.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
DR   EMBL; M84163; XLPPARG.
DR   PIR; C42214; C42214.
DR   HSSP; P10826; 1HRA.
DR   TRANSFAC; T01354; -.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND     113    177       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      113    133       C4-TYPE.
FT   ZN_FING      150    172       C4-TYPE.
FT   DOMAIN       293    477       LIGAND-BINDING (POTENTIAL).
SQ   SEQUENCE   477 AA;  54055 MW;  1113537 CN;

  DB  6;  Score    2579;  Match 73.9%;  QryMatch 71.4%;  Pred. No. 0.00e+00;
  Matches   357;  Conservative   62;  Mismatches  50;  Indels  14;  Gaps  10;

Db      1 mvdtempfwsnlnfgmnsmdmsaledhcqpydikpfttvdfssins-hyddildektflc 59
          |||||||||:  |||::|:|:| :||| :::||||||||||||:: ||:||     |
Qy     20 MVDTEMPFWPT-NFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDI----PFT- 73

Db     60 rndqspidykydlklqecqssikleppsppyfsdkpq-cskafedtpnsfiaiecrvcgd 118
          | |    |||||||||| ||:||:||:||||:|:| |  :|: |: :||::|||||||||
Qy     74 RTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGD 133

Db    119 kasgfhygvhacegckgffrrtirlkliyercdlncrihkksrnkcqfcrfqkclavgms 178
          ||||||||||||||||||||||||||||:||||||||||||||||:||||||||||||
Qy    134 KASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMS 193

Db    179 hnairfgrmpqaekekllaeissdidqlnpesadqrvlakhlydsyvksfpltkakapgh 238
          |||||||||||||||||||||||||||||||| | |||||||||:|||||||||| :
Qy    194 HNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAI 253

Db    239 pdgqshrqnsrgytrheladdgggsdqgavre-praeqgggdsnlpal-svalrg--gvr 294
            | :  ::|  :   ::     | |    :     :: : :  :  : :  :|:  :|:
Qy    254 LTGKT-TDKSP-FVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQ 311

Db    295 eitefaknipgfvsldlndqvtllkygvheiiftmlaslmnkdgvlvaeqqgfmtreflk 354
          ||||:|||:|||||:|||||||||||||||||:||||||||||||::|||||||||||
Qy    312 EITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLK 371

Db    355 slrkpfsdfmepkfefairfnslelddsdlaifvaviilsgdrpgllnvkpiediqdsll 414
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          ||||||:||||||||||::||:||||||||||:|||||||||||||||||||||||||:||
Qy    372 SLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLL 431

Db    415 qalelqlklnhpdsaqlfakllqkmtdlrqvvtehvqllqlikkteadmclhpllqeiyk 474
          ||||||||||||:|:|||||||||||||||:|||||||||:|||||:|| ||||||||||
Qy    432 QALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYK 491

Db    475 dly 477
          |||
Qy    492 DLY 494


RESULT    4
ID   PPAR_HUMAN     STANDARD;      PRT;   468 AA.
AC   Q07869;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA).
GN   PPARA OR PPAR.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RM   93277839
RA   SHER T., YI H.F., MCBRIDE O.W., GONZALES F.J.;
RL   BIOCHEMISTRY 32:5598-5604(1993).
CC   -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC       HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC       THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC       OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC       PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
DR   EMBL; L02932; HSPPAR.
DR   PIR; A49289; A49289.
DR   HSSP; P10826; 1HRA.
DR   MIM; 170998; 11TH EDITION.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND     102    166       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      102    122       C4-TYPE.
FT   ZN_FING      139    161       C4-TYPE.
FT   DOMAIN       281    468       LIGAND-BINDING (POTENTIAL).
SQ   SEQUENCE   468 AA;  52267 MW;  1083954 CN;

  DB  6;  Score    1946;  Match 65.2%;  QryMatch 53.8%;  Pred. No. 0.00e+00;
  Matches   247;  Conservative   78;  Mismatches  51;  Indels   3;  Gaps   3;

Db     92 espsgal-niecricgdkasgyhygvhacegckgffrrtirlklvydkcdrsckiqkknr 150
          | || :|  ||||:||||||||:|||||||||||||||||||||||:||:|| :|:|:||:|
Qy    117 EEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSR 176

Db    151 nkcqycrfhkclsvgmshnairfgrmprsekaklkaeiltcehdiedsetadlkslakri 210
          ||||||||:|||:|||||||||||||||::|| || ||| : : |  ::|:|||::||||::
Qy    177 NKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHL 235

Db    211 yeaylknfnmnkvkarvilsgkasnnppfvihdmetlcmaektlvaklvan-giqnkeve 269
          |::|:|:| : | ||| ||:||:::::|||| ||::| |:|  :  | ::    |:|||
Qy    236 YDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVA 295
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Db    270 vrifhccqctsvetvteltefakaipafanldlndqvtllkygvyeaifamlssvmnkdg 329
          :|||: ||  |||:| |:||:||:||:| |||||||||||||| | |::||:|:|||||
Qy    296 IRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDG 355

Db    330 mlvaygngfitreflkslrkpfcdimepkfdfamkfnalelddsdislfvaaiiccgdrp 389
          :|:: | ||:|||||||||||| |:|||||:||:|||||||||||:::|:| ||  |||
Qy    356 VLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRP 415

Db    390 gllnvghiekmqegivhvlrlhlqsnhpddiflfpkllqkmadlrqlvtehaqlvqiikk 449
          |||||  || :|: ::: | |:|  |||:   ||:||||||:||||:|||| ||:|:|||
Qy    416 GLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKK 475

Db    450 tesdaalhpllqeiyrdmy 468
          ||:| :||||||||:|:|
Qy    476 TETDMSLHPLLQEIYKDLY 494


RESULT    5
ID   PPAR_MOUSE     STANDARD;      PRT;   468 AA.
AC   P23204;
DT   01-NOV-1991 (REL. 20, CREATED)
DT   01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA).
GN   PPARA OR PPAR.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   91015382
RA   ISSEMANN I., GREEN S.;
RL   NATURE 347:645-650(1990).
CC   -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC       HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC       THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC       OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC       PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC   -!- DISEASE: PEROXISOME PROLIFERATORS ARE A DIVERSE GROUP OF
CC       CHEMICALS THAT INCLUDE HYPOLIPIDAEMIC DRUGS, HERBICIDES AND
CC       INDUSTRIAL PLASTICISERS. ADMINISTRATION OF THESE CHEMICALS TO
CC       RODENTS RESULTS IN THE DRAMATIC PROLIFERATION OF HEPATIC
CC       PEROXISOMES AS WELL AS LIVER HYPERPLASIA.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER, KIDNEY AND
CC       HEART. VERY WEAKLY EXPRESSED IN BRAIN AND TESTIS.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
DR   EMBL; X57638; MMPPAR.
DR   PIR; S11659; S11659.
DR   HSSP; P10826; 1HRA.
DR   TRANSFAC; T00694; -.
DR   PROSITE; PS00031; STEROID_FINGER.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND     102     166       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      102     122       C4-TYPE.
FT   ZN_FING      139     161       C4-TYPE.
FT   DOMAIN       281     468       LIGAND-BINDING (POTENTIAL).
SQ   SEQUENCE   468 AA;  52432 MW;  1094992 CN;

  DB  6;  Score    1932;  Match 64.6%;  QryMatch 53.5%;  Pred. No. 0.00e+00;
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  Matches   245;  Conservative   79;  Mismatches  53;  Indels   2;  Gaps   2;

Db     91 despgsalniecricgdkasgyhygvhacegckgffrrtirlklvydkcdrsckiqkknr 150
          :|:: | : ||||:|||||||:|||||||||||||||||||||:||:|| :|:|:|||:|
Qy    117 EEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSR 176

Db    151 nkcqycrfhkclsvgmshnairfgrmprsekaklkaeiltcehdlkdsetadlkslgkri 210
          ||||||||:|||:|||||||||||||::|| || ||| : : |  ::|:|||::|:|::
Qy    177 NKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHL 235

Db    211 heaylknfnmnkvkarvilagktsnnppfvihdmetlcmaektlvakmvangved-keae 269
            ::|:|:| : | ||| ||:|||:::|||| ||::| |:|  :  | ::   |: ||
Qy    236 YDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVA 295

Db    270 vrffhccqcmsvetvteltefakaipgfanldlndqvtllkygvyeaiftmlsslmnkdg 329
          :|:|: ||  |||:| |:||:||:|||| ||||||||||||||| | |:|||:|||||||
Qy    296 IRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDG 355

Db    330 mliaygngfitreflknlrkpfcdimepkfdfamkfnalelddsdislfvaaiiccgdrp 389
          :||: | ||:||||||:|||| |:|||||:||:|||||||||||:::|:| ||  ||||
Qy    356 VLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRP 415

Db    390 gllnigyieklqegivhvlklhlqsnhpddtflfpkllqkmvdlrqlvtehaqlvqvikk 449
          ||||:  || :|: ::: | |:|  |||: : ||:|||||| ||||:|||| ||:|||||
Qy    416 GLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKK 475

Db    450 tesdaalhpllqeiyrdmy 468
          ||:| :||||||||:|:|
Qy    476 TETDMSLHPLLQEIYKDLY 494


RESULT    6
ID   PPAR_RAT       STANDARD;      PRT;   468 AA.
AC   P37230;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA).
GN   PPARA OR PPAR.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92262498
RA   GOETTLICHER M., WIDMARK E., LI Q., GUSTAFSSON J.A.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 89:4653-4657(1992).
CC   -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC       HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC       THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC       OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC       PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
DR   EMBL; M88592; RNPPAR.
DR   PIR; A45288; A45288.
DR   HSSP; P10826; 1HRA.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND     102     166       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      102     122       C4-TYPE.
FT   ZN_FING      139     161       C4-TYPE.
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FT   DOMAIN      281    468       LIGAND-BINDING (POTENTIAL).
SQ   SEQUENCE   468 AA;  52377 MW;  1090484 CN;

  DB  6;  Score    1930;  Match 65.2%;  QryMatch 53.4%;  Pred. No. 0.00e+00;
  Matches   247;  Conservative   76;  Mismatches  53;  Indels   3;  Gaps   3;

Db     92 espgnal-niecricgdkasgyhygvhacegckgffrrtirlklaydkcdrsckiqkknr 150
           | ||:|:|  ||||:|||||||:||||||||||||||||||||| ||:|| :|:|:||:|
Qy    117 EEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSR 176

Db    151 nkcqycrfhkclsvgmshnairfgrmprsekaklkaeiltcehdlkdsetadlkslakri 210
           ||||||||:|||:|||||||||||||||::|| || ||| : : |  ::|:|||::|||::
Qy    177 NKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHL 235

Db    211 heaylknfnmnkvkarvilagktsnnppfvihdmetlcmaektlvakmvan-gvenkeae 269
            ::|:|:| : | ||| ||:|||::::|||| ||::| |:|  :  | ::    ::||
Qy    236 YDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVA 295

Db    270 vrffhccqcmsvetvteltefakaipgfanldlndqvtllkygvyeaiftmlsslmnkdg 329
           :|:|: ||  |||:| |:||:||:|||| ||||||||||||| | |:|||:|||||||
Qy    296 IRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDG 355

Db    330 mliaygngfitreflknlrkpfcdimepkfdfamkfnalelddsdislfvaaiiccgdrp 389
           :||: | ||:|||||:||||| |:|||||:||:|||||||||||:::|:| ||  ||||
Qy    356 VLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRP 415

Db    390 gllnigyieklqegivhvlklhlqsnhpddtflfpkllqkmvdlrqlvtehaqlvqvikk 449
           ||||:  || :|: ::: | |:|  |||: : ||:|||||| ||||:|||| ||:|||||
Qy    416 GLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKK 475

Db    450 tesdaalhpllqeiyrdmy 468
           ||:| :|||||||||:|:|
Qy    476 TETDMSLHPLLQEIYKDLY 494


RESULT    7
ID   PPAS_HUMAN     STANDARD;      PRT;   441 AA.
AC   Q03181;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA).
GN   PPARB.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   93078797
RA   SCHMIDT A., ENDO N., RUTLEDGE S.J., VOGEL R., SHINAR D.,
RA   RODAN G.A.;
RL   MOL. ENDOCRINOL. 6:1634-1641(1992).
CC   -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC       HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC       THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC       OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC       PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
DR   EMBL; L07592; HSPPARA.
DR   PIR; A45360; A45360.
DR   HSSP; P10826; 1HRA.
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DR   PROSITE; PS00031; STEROID_FINGER.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND     74    138       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      74     94       C4-TYPE.
FT   ZN_FING     111    133       C4-TYPE.
FT   DOMAIN      254    441       LIGAND-BINDING (BY SIMILARITY).
SQ   SEQUENCE   441 AA;  49903 MW;  973846 CN;

  DB  6;  Score    1921;  Match 65.6%;  QryMatch 53.2%;  Pred. No. 0.00e+00;
  Matches   244;  Conservative   79;  Mismatches  48;  Indels   1;  Gaps   1;

Db     70 lnmecrvcgdkasgfhygvhacegckgffrrtirmkleyekcersckiqkknrnkcqycr 129
           : :|||||||||||||||||||||||||||||||||:|| |::|: :|:|:||:||||||||
Qy    124 MAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCR 183

Db    130 fqkclalgmshnairfgrmpeaekrklvaqltanegsqynpqvadlkafskhiynaylkn 189
           ||||||:|||||||||||||:||| ||:| ::::   | ||: |||:|::||:|::|:|:
Qy    184 FQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDID-QLNPESADLRALAKHLYDSYIKS 242

Db    190 fnmtkkkarsiltgkashtapfvihdietlwqaekglvwkqlvnglppykeisvhvfyrc 249
           | :|| |||:|||||::  :|||| |:::|  :|  :  |::       ||:::::|  |
Qy    243 FPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGC 302

Db    250 qcttvetvreltefaksipsfsslflndqvtllkygvheaifamlasivnkdgllvangs 309
           |  :||:|:|:||:|||||:| :| ||||||||||||||| |::|||||::||||:|:::|
Qy    303 QFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQ 362

Db    310 gfvtreflrslrkpfsdiiepkfefavkfnalelddsdlalfiaaiilcgdrpglmnvpr 369
           ||:|||||:|||||:|::|||||||||||||||||||||:||| ||| |||||||:||
Qy    363 GFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKP 422

Db    370 veaiqdtilralefhlqanhpdaqylfpkllqkmadlrqlvtehaqmmqrikktetetsl 429
           :| ||| :|:|||::|  ||||:  ||:|||||||:||||:|||| |::| ||||||: ||
Qy    423 IEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSL 482

Db    430 hpllqeiykdmy 441
           ||||||||||:|
Qy    483 HPLLQEIYKDLY 494


RESULT    8
ID   PPAR_XENLA     STANDARD;      PRT;   474 AA.
AC   P37232;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA).
GN   PPARA.
OS   XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92191267
RA   DREYER C., KREY G., KELLER H., GIVEL F., HELFTENBEIN G., WAHLI W.;
RL   CELL 68:879-887(1992).
RN   [2]
RP   CHARACTERIZATION.
RM   94100165
RA   KREY G., KELLER H., MAHFOUDI A., MEDIN J., OZATO K., DREYER C.,
RA   WAHLI W.;
RL   J. STEROID BIOCHEM. MOL. BIOL. 47:65-73(1993).
CC   -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC       HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
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CC       THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC       OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC       PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC   -!- DEVELOPMENTAL STAGE: OOCYTES, EMBRYOS, AND ADULTS
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
DR   EMBL; M84161; XLPPARA.
DR   PIR; A42214; A42214.
DR   HSSP; P10826; 1HRA.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND     109    173       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      109    129       C4-TYPE.
FT   ZN_FING      146    168       C4-TYPE.
FT   DOMAIN       287    474       LIGAND-BINDING (POTENTIAL).
SQ   SEQUENCE   474 AA;  52856 MW;  1122618 CN;

  DB  6;  Score    1894;  Match 64.8%;  QryMatch 52.4%;  Pred. No. 0.00e+00;
  Matches   247;  Conservative   74;  Mismatches  56;  Indels   4;  Gaps   4;

Db      97 aedaacksl-nlecrvcsdkasgfhygvhacegckgffrrtirlklvydrcermckiqkk 155
           : : : :|| :|||||:||||||||||||||||||||||||||||:||||:  |:|:||
Qy     115 PHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKK 174

Db     156 nrnkcqycrfekclnvqmshnairfgrmprsekaklkaevlmcdqdvkdsqmadllslar 215
           :|||||||||:||| ||||||||||||||::|| || ||:   | |  ::: ||| :||:
Qy     175 SRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAK 233

Db     216 liydaylknfnmnkvkarailtgkasn-ppfvihdmetlcmaektlvaklvan-giqnke 273
           :||:|:|:| : | |||||||||::: :|||| ||::| |:|  :  | ::    |:||
Qy     234 HLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKE 293

Db     274 aevrifhccqctsvetvteltefaksipgfteldlndqvtllkygvyeamfamlasvmnk 333
             :|||: ||  |||:| |:||:|||||| :|||||||||||| | :::||||:|||
Qy     294 VAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNK 353

Db     334 dgmlvaygngfitreflkslrkpigdmmepkfefamkfnalelddsdlslfvaaliccgd 393
           ||:|:: | ||:|||||||||:|| |||||||:|||||||||||::|:| :|  ||
Qy     354 DGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGD 413

Db     394 rpglvnipsiekmqesivhvlklhlqsnhpddsflfpkllqkmadlrqlvtehaqlvqti 453
           ||||:|: :|| :|:::::: | |:|  |||: | ||:||||||:||||:|||| ||:| |
Qy     414 RPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVI 473

Db     454 kktetdaalhpllqeiyrdmy 474
           |||||| :||||||||:|:|
Qy     474 KKTETDMSLHPLLQEIYKDLY 494


RESULT    9
ID   PPAS_MOUSE     STANDARD;      PRT;   440 AA.
AC   P35396;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA).
GN   PPARB.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=ADIPOCYTE;
RA   AMRI E.-Z., BONINO F., AILHAUD G., GRIMALDI P.;
RL   SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC       HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC       THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC       OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC       PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
DR   EMBL; L28116; MMPPARA.
DR   HSSP; P10826; 1HRA.
DR   PROSITE; PS00031; STEROID_FINGER.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND      73    137       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING       73     93       C4-TYPE.
FT   ZN_FING      110    132       C4-TYPE.
FT   DOMAIN       253    440       LIGAND-BINDING (POTENTIAL).
SQ   SEQUENCE   440 AA;  49715 MW;  980155 CN;

  DB  6;  Score    1886;  Match 63.6%;  QryMatch 52.2%;  Pred. No. 0.00e+00;
  Matches   241;  Conservative   84;  Mismatches  53;  Indels   1;  Gaps   1;

Db      62 dgasggslnmecrvcgdkasgfhygvhacegckgffrrtirmkleyekcdrickiqkknr 121
           : :| : : :|||||||||||||||||||||||||||||||:|| |::||  |:|:||:|
Qy     117 EEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSR 176

Db     122 nkcqycrfqkclalgmshnairfgrmpeaekrklvagltaseqcqhnpqladlkafskhi 181
           ||||||||||||:|||||||||||||:||| ||:| :::    | ||: |||:|::||:
Qy     177 NKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDID-QLNPESADLRALAKHL 235

Db     182 ynaylknfnmtkkkarsiltgksshnapfvihdietlwqaekglvwkqlvnglppyneis 241
           |::|:|:| :|| |||:|||||:: ::|||| |:::|  :|  :  |::        :|::
Qy     236 YDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVA 295

Db     242 vhvfyrcqsttvetvreltefaknipnfsslflndqvtllkygvheaifamlasivnkdg 301
           :::|  ||  :|||:|:|:||:||:|| | :| ||||||||||||| |::||||::||||
Qy     296 IRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDG 355

Db     302 llvangsgfvtheflrslrkpfsdiiepkfefavkfnalelddsdlalfiaaiilcgdrp 361
           :|:::| ||:|:|||:|||||:|::|||||||||||||||||||:||| ||| ||||
Qy     356 VLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRP 415

Db     362 glmnvpqveaiqdtilralefhlqvnhpdsqylfpkllqkmadlrqlvtehaqmmqwlkk 421
           ||:||  :| ||| :|:|||::| :|||:|  ||:||||||:||||:|||| |::| :||
Qy     416 GLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKK 475

Db     422 tesetllhpllqeiykdmy 440
           ||::  ||||||||||:|
Qy     476 TETDMSLHPLLQEIYKDLY 494


RESULT   10
ID   PPAS_XENLA     STANDARD;      PRT;   396 AA.
AC   P37233;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA).
GN   PPARB.
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OS   XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92191267
RA   DREYER C., KREY G., KELLER H., GIVEL F., HELFTENBEIN G., WAHLI W.;
RL   CELL 68:879-887(1992).
RN   [2]
RP   CHARACTERIZATION.
RM   94100165
RA   KREY G., KELLER H., MAHFOUDI A., MEDIN J., OZATO K., DREYER C.,
RA   WAHLI W.;
RL   J. STEROID BIOCHEM. MOL. BIOL. 47:65-73(1993).
CC   -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC       HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC       THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC       OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC       PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC   -!- DEVELOPMENTAL STAGE: OOCYTES, EMBRYOS, AND ADULTS
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
DR   EMBL; M84162; XLPPARB.
DR   PIR; B42214; B42214.
DR   HSSP; P10826; 1HRA.
DR   TRANSFAC; T01353; -.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND     31     95       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      31     51       C4-TYPE.
FT   ZN_FING      68     90       C4-TYPE.
FT   DOMAIN      209    396       LIGAND-BINDING (POTENTIAL).
SQ   SEQUENCE   396 AA;  44991 MW;  780125 CN;

  DB  6;  Score    1743;  Match 57.9%;  QryMatch 48.2%;  Pred. No. 1.37e-303;
  Matches   221;  Conservative   79;  Mismatches  80;  Indels   2;  Gaps   2;

Db     17 stplehqets-qsvdckicgdrasgfhygvhacegckgffrrtirmrlqyehcdrnckiq 75
          : | |    |  :::|::|||:|||||||||||||||||||||||::| |::|| ||:|:
Qy    113 NKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIH 172

Db     76 kknrnkcqycrfnkclslgmshnairfgrmpesekrklvqapvsdsaapdspvsdldvls 135
          ||:|||||||| |||::|||||||||||||::|| ||:    ||    ::  :|| |:
Qy    173 KKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALA 232

Db    136 qlihssymntftmtkkrardiltgrns-ispfvihdmdtlwqaeqgtvweqlptqnltgt 194
             :  ||:::| :|| :|| |||| : : ||||| ||::|  :|:     ::      :
Qy    233 KHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSK 292

Db    195 eiqvhvfyrcqctsvetvraltdfakripgfgtlylndqvtllkygvheaifcmlaslmn 254
          |:::::|  ||  |||:|: :|::|| |||| | ||||||||||||| |: |||||||
Qy    293 EVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMN 352

Db    255 kdgllvaggrgfvtreflrslrqpfchimepkfhfaskfnalelndsdlalfvasiilcg 314
          |||:|:: |:||:|||||:||| ||  :||||| || |||||||:|||||:|:| ||| |
Qy    353 KDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSG 412

Db    315 drpglinpsqvediqegilgalrrhlkashtdapflfpkllhkmadlrqlvtehaelvqs 374
          |||||:|   :||||: :| ||  :|| :| ::: ||:|||:||:||||:|||| :|:|
Qy    413 DRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQV 472

Db    375 ikrtessaalhpllqeiyrdmy 396
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          ||:||:  :|||||||||:|:|
Qy    473 IKKTETDMSLHPLLQEIYKDLY 494


RESULT   11
ID   E75A_DROME     STANDARD;      PRT;  1237 AA.
AC   P17671;
DT   01-AUG-1990 (REL. 15, CREATED)
DT   01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   ECDYSONE-INDUCIBLE PROTEIN E75-A.
GN   EIP75B.
OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CANTON-S;
RM   90249727
RA   SEGRAVES W.A., HOGNESS D.S.;
RL   GENES DEV. 4:204-219(1990).
CC   -!- FUNCTION: IMPLICATED IN THE REGULATION OF ECDYSONE-TRIGGERED
CC       GENE HIERARCHIES. PROBABLY PLAYS A KEY ROLE IN MEDIATING THE
CC       REGULATION OF THE LARVAL MOLT BY 20-OH-ECDYSONE.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC   -!- INDUCTION: THE EXPRESSION OF THIS PROTEIN IS DEVELOPMENTALLY
CC       REGULATED AND IS CORRELATED WITH THE 20-OH-ECDYSONE INDUCED
CC       ACTIVITY OF PUFF 75B.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF PROTEIN E75 ARE
CC       PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
DR   EMBL; X51548; DME75A.
DR   PIR; A34598; A34598.
DR   HSSP; P10826; 1HRA.
DR   TRANSFAC; T01367; -.
DR   FLYBASE; FBGN0000568; EIP75B.
DR   PROSITE; PS00031; STEROID_FINGER.
KW   RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW   ZINC-FINGER; ALTERNATIVE SPLICING.
FT   DNA_BIND     245    311       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      245    265       C4-TYPE.
FT   ZN_FING      282    306       C4-TYPE.
FT   DOMAIN       721    729       POLY-GLN.
FT   DOMAIN      1049   1077       POLY-SER.
SQ   SEQUENCE   1237 AA;  133331 MW;  7722251 CN;

  DB  2;  Score     706;  Match 34.1%;  QryMatch 19.5%;  Pred. No. 6.45e-103;
  Matches   123;  Conservative   92;  Mismatches 127;  Indels  19;  Gaps  17;

Db    242 tvlcrvcgdkasgfhygvhscegckgffrrsiqqkiqyrpctknqqcsilrinrnrcqyc 301
          :: |||||||||||||||:|||||||||||:|: |: |  |  :  | | : :||:||||
Qy    125 AIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRC--DLNCRIHKKSRNKCQYC 182

Db    302 rlkkciavgmsrdavrfgrvpkrekarilaamqqst-q-nr-gqq-ralatel-ddqprl 356
          |: ||:|||||::|:||||:|  || ::|| :     | |  : : ||||  | |   :
Qy    183 RFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKS 242

Db    357 la-avlrahletceftkekvs-amrqrardcpsysmptl-lacplnpapelqseqef-s- 411
          :: :  :|:      | :| :  : :      :  :  :    ||   :   : : | :
Qy    243 FPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGC 302

Db    412 q-rfahvirgvidfagmipgfqlltqddkftllkaglfdalfvrlicmfdssinsiicln 470
          | |    :: : ::|  ||||  |  :|  |||| |: : ::  |  : :     :|  :
Qy    303 QFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKD-GVLIS-E 360
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Db    471 gqv-mrrdaiqnganarf--lvdstfnfaermnsmnltdaeiglfcaivlitpdrpglrn 527
          ||  | |: : ::    |  :::: |:|| : |:::| |::::::| |::::: ||||| |
Qy    361 GQGFMTRE-FLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLN 419

Db    528 leliekmysrlkgclqyivaqnrpdqpeflaklletmpdlrtlstlhteklvvfrtehke 587
          :  || :   |   |:  :  |:|: ::::||||: | ||| : | | : | |::    :
Qy    420 VKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETD 479

Db    588 l 588
          :
Qy    480 M 480


RESULT   12
ID   E75C_DROME     STANDARD;      PRT;  1443 AA.
AC   P13055;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   ECDYSONE-INDUCIBLE PROTEIN E75-C.
GN   EIP75B.
OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CANTON-S; TISSUE=HEAD;
RM   90016778
RA   FEIGL G., GRAM M., PONGS O.;
RL   NUCLEIC ACIDS RES. 17:7167-7178(1989).
CC   -!- FUNCTION: IMPLICATED IN THE REGULATION OF ECDYSONE-TRIGGERED
CC       GENE HIERARCHIES. PROBABLY PLAYS A KEY ROLE IN MEDIATING THE
CC       REGULATION OF THE LARVAL MOLT BY 20-OH-ECDYSONE.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC   -!- INDUCTION: THE EXPRESSION OF THIS PROTEIN IS DEVELOPMENTALLY
CC       REGULATED AND IS CORRELATED WITH THE 20-OH-ECDYSONE INDUCED
CC       ACTIVITY OF PUFF 75B.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF PROTEIN E75 ARE
CC       PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
DR   EMBL; X15586; DM75B.
DR   PIR; S05979; S05979.
DR   HSSP; P10826; 1HRA.
DR   FLYBASE; FBGN0000568; EIP75B.
DR   PROSITE; PS00031; STEROID_FINGER.
KW   RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW   ZINC-FINGER; ALTERNATIVE SPLICING.
FT   DNA_BIND     454    520       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      454    474       C4-TYPE.
FT   ZN_FING      491    515       C4-TYPE.
SQ   SEQUENCE   1443 AA;  156265 MW;  10403942 CN;

  DB  2;  Score     641;  Match 34.2%;  QryMatch 17.7%;  Pred. No. 9.62e-91;
  Matches   124;  Conservative   88;  Mismatches 126;  Indels  25;  Gaps  23;

Db    451 tvlcrvcgdkasgfhygvhscegckgffrrsiqqkiqyrpctknqqcsilrinrnrcqyc 510
          :: |||||||||||||||||:||||||||||:|: |: |  |  :  | | : :||:|||| |
Qy    125 AIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRC--DLNCRIHKKSRNKCQYC 182

Db    511 rlkkciavgmsrdavrfgrvpkrekariwrpcnra-priaa-ssd-psppswm-tshass 566
          |: ||:||||||::|:||||:|  || ::    :    :: : |:|  : :  :  |   |
Qy    183 RFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKS 242
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Db    567 -ppccc-ah-letceft-kek-vs-amrh-grglpstpc-htsglsaepapelqseqef- 617
          |    |: : |  | |  |  |     |       | : |  | : |: : : |
Qy    243 FPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPL-QEQSKEV-AIRIFQ 300

Db    618 s-q-rfahvirgvidfaqmipgfqlltqddkftllkaglfdalfvrlicmfdssinsiic 675
          : | |   :: : ::|  |||| |  :|  |||| |: : ::  |  : :     :|
Qy    301 GCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKD-GVLIS 359

Db    676 lngqv-mrrdaiqnganarf--lvdstfnfaermnsmnltdaeiglfcaivlitpdrpgl 732
          :||  | |: : ::    |  :::: |:|| : |:::| |::::::| |::::: ||||| |
Qy    360 -EGQGFMTRE-FLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGL 417

Db    733 rnleliekmysrlkgclqyivaqnrpdqpeflaklletmpdlrtlstlhteklvvfrteh 792
          |:  ||  :   |   |:  :  |:|: ::::||||: | ||| : | | : | |::
Qy    418 LNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTE 477

Db    793 kel 795
          ::
Qy    478 TDM 480


RESULT   13
ID   PPAU_MOUSE     STANDARD;      PRT;   158 AA.
AC   P37239;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR NUC1 (PPAR-NUC1)
DE   (FRAGMENT).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=BRAIN;
RM   94059089
RA   CHEN F., LAW S.W., O'MALLEY B.W.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 196:671-677(1993).
CC   -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC       HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC       THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC       OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC       PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
DR   EMBL; U01665; MM665.
DR   HSSP; P10826; 1HRA.
KW   RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW   NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT   DNA_BIND      86    150       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING       86    106       C4-TYPE.
FT   ZN_FING      123    145       C4-TYPE.
FT   NON_TER      158    158
SQ   SEQUENCE   158 AA;  17316 MW;  110700 CN;

  DB  6;  Score     558;  Match 77.4%;  QryMatch 15.4%;  Pred. No. 2.36e-75;
  Matches    65;  Conservative   12;  Mismatches   7;  Indels   0;  Gaps   0;

Db     75 dgasggslnmecrvcgdkasgfhygvhacegckgffrrtirmkleyekcdrickiqkknr 134
          : :| : : :|||||||||||||||||||||||||||||||||:|| |::||  |:|:||:|
Qy    117 EEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSR 176
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Db    135 nkcqycrfqkclalgmshnairfg 158
          ||||||||||||||:||||||||||
Qy    177 NKCQYCRFQKCLAVGMSHNAIRFG 200


RESULT   14
ID   E75B_DROME     STANDARD;      PRT;  1394 AA.
AC   P17672;
DT   01-AUG-1990 (REL. 15, CREATED)
DT   01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   ECDYSONE-INDUCIBLE PROTEIN E75-B.
GN   EIP75B.
OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CANTON-S;
RM   90249727
RA   SEGRAVES W.A., HOGNESS D.S.;
RL   GENES DEV. 4:204-219(1990).
CC   -!- FUNCTION: IMPLICATED IN THE REGULATION OF ECDYSONE-TRIGGERED
CC       GENE HIERARCHIES. PROBABLY PLAYS A KEY ROLE IN MEDIATING THE
CC       REGULATION OF THE LARVAL MOLT BY 20-OH-ECDYSONE.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC   -!- INDUCTION: THE EXPRESSION OF THIS PROTEIN IS DEVELOPMENTALLY
CC       REGULATED AND IS CORRELATED WITH THE 20-OH-ECDYSONE INDUCED
CC       ACTIVITY OF PUFF 75B.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS BUT LACK THE DNA-BINDING REGION.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF PROTEIN E75 ARE
CC       PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
DR   EMBL; X51549; DME75B.
DR   PIR; B34598; B34598.
DR   HSSP; P10826; 1HRA.
DR   TRANSFAC; T01368; -.
DR   FLYBASE; FBGN0000568; EIP75B.
KW   RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW   ZINC-FINGER; ALTERNATIVE SPLICING.
SQ   SEQUENCE   1394 AA;  152097 MW;  9605497 CN;

  DB  2;  Score     528;  Match 30.4%;  QryMatch 14.6%;  Pred. No. 7.64e-70;
  Matches   105;  Conservative   90;  Mismatches 131;  Indels  19;  Gaps  17;

Db    415 avtanedadgffrrsiqqkiqyrpctknqqcsilrinrnrcqycrlkkciavgmsrdavr 474
          :| | |   |||||:|: |: |  |  :  | | : :||:|||||: ||:|||||::|:|
Qy    141 GVHACEGCKGFFRRTIRLKLIYDRC--DLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIR 198

Db    475 fgrvpkrekarilaamqqst-q-nr-gqq-ralatel-ddqprlla-avlrahletceft 528
          |||:|  || ::|| :     | |  : : |||| | |   : :: :  :|:      |
Qy    199 FGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKT 258

Db    529 kekvs-amrqrardcpsysmptl-lacplnpapelqseqef-s-q-rfahvirgvidfag 583
          :| :  : :       :  :  :    ||   :  : : | : | |    :: : ::|
Qy    259 TDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAK 318

Db    584 mipgfqlltqddkftllkaglfdalfvrlicmfdssinsiiclngqv-mrrdaiqngana 642
          ||||  |  :|  |||| |: : ::  |  : :     :|  :||  | |: : ::
Qy    319 SIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKD-GVLIS-EGQGFMTRE-FLKSLRK 375

Db    643 rf--lvdstfnfaermnsmnltdaeiglfcaivlitpdrpglrnleliekmysrlkgclq 700
          |  :::: |:|| : |:::| |:::::| |::::: ||||| |:  || :   |   |:
Qy    376 PFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALE 435
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Db    701 yivaqnrpdqpeflaklletmpdlrtlstlhteklvvfrtehkel 745
          :  |:|: ::::|||||: | ||| : | | : | |::    ::
Qy    436 LQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDM 480


RESULT   15
ID   THB1_XENLA     STANDARD;      PRT;   369 AA.
AC   P18116;
DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   THYROID HORMONE RECEPTOR BETA-A1.
OS   XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   90384953
RA   YAOITA Y., SHI Y.-B., BROWN D.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 87:7090-7094(1990).
RN   [2]
RP   ERRATUM.
RM   91046059
RA   YAOITA Y., SHI Y.-B., BROWN D.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 87:8684-8684(1990).
CC   -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR TRIIODOTHYRONINE.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC       A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC       NUCLEAR HORMONE RECEPTORS.
CC   -!- ALTERNATIVE PRODUCTS: SPLICING OF THE BETA-A GENE PRODUCES
CC       VARIANTS OF THE RECEPTOR.
DR   EMBL; M35359; XLBETA.
DR   PIR; C36067; C36067.
DR   HSSP; P10826; 1HRA.
DR   PROSITE; PS00031; STEROID_FINGER.
KW   RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
KW   ZINC-FINGER; MULTIGENE FAMILY; ALTERNATIVE SPLICING.
FT   DOMAIN       1     14       MODULATING (POTENTIAL).
FT   DNA_BIND     15    82       C4-TYPE ZINC FINGERS (TWO).
FT   ZN_FING      15    35       C4-TYPE.
FT   ZN_FING      53    77       C4-TYPE.
FT   DOMAIN      132   369       LIGAND-BINDING.
SQ   SEQUENCE   369 AA;  41939 MW;  691170 CN;

  DB  7;  Score     525;  Match 31.4%;  QryMatch 14.5%;  Pred. No. 2.71e-69;
  Matches   117;  Conservative   99;  Mismatches 131;  Indels  26;  Gaps  25;

Db     15 cvvcgdkatgyhyrcitcegckgffrrtiqknlhpsysckyegkcvidkvtrnqcqecrf 74
          | ||||||:|:||   :||||||||||||| : |   |  : : :| | | :|| || |||
Qy    128 CRVCGDKASGFHYGVHACEGCKGFFRRTI-R-LKLIYD-RCDLNCRIHKKSRNKCQYCRF 184

Db     75 kkciavgmatdlv-lddnkrlakrkliee-nre-krrkde-iq-kslvqkp-eptqeewe 128
          ||:|||||: : : :    :  | ||: | : :  : : |  : ::|     ::
Qy    185 QKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFP 244

Db    129 liqvvteahvatnaqg-shw-k-qkrkfl-ped-igqapivnapeggk-vdleaf-s-qf 180
          |    : | :: ::   |     ::  ::  || |    |    | :| | :  | : ||
Qy    245 LTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQF 304

Db    181 tkiitpaitrvvdfakklpmfcelpcedqiillk-gccmeimslraavrydpesetltln 239
          : :  |:  : ::|| :| | :|  :||: ||| |    | :: |::  : ::  |  :
Qy    305 -RSVE-AVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLM-NKDG-VLISE 360
```

```
Db    240 gemavtrgqlkn--gglgvvsdaifdlgvslssfslddtevallqavllmssdrpglasv 297
          |:  :||  ||:    :|   :: |:::| :::: |||:::|:: ||:::|:|||| :|
Qy    361 GQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNV 420

Db    298 eriekcqegfllafehyinyrkhniahfwpkllmkvtdlrmigachasrflhmkvecpte 357
            ||  |: :| |:|  ::    : ::: :||| |:|||| | : |  ::|::     |:
Qy    421 KPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHV-QLLQVIKKTETD 479

Db    358 l-fpplflevfed 369
          : : ||: |:: |
Qy    480 MSLHPLLQEIYKD 492

Search completed: Fri Nov 17 08:30:52 1995
Job time : 15 secs.
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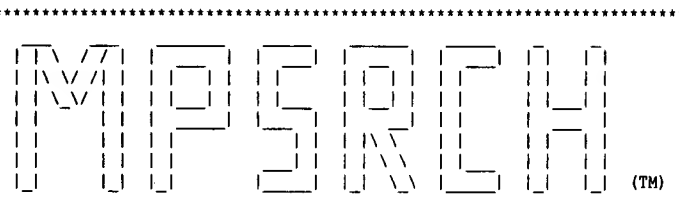


Release 2.1D John F. Collins, Biocomputing Research Unit.


MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Nov 17 08:31:10 1995; MasPar time 19.96 Seconds
590.346 Million cell updates/sec

Tabular output not generated.

Title: US-08-380-051-2
Description: (1:494) from US08380051.pep
Perfect Score: 3614
Sequence: 1 MLKLIVPFLKRESAFNEMTM.....KTETDMSLHPLLQEIYKDLY 494

Scoring table: PAM 150
Gap 11

Searched: 78488 seqs, 23849247 residues

Database: pir45
1 ann1
2 ann2
3 ann3
4 unann1
5 unann2
6 unann3
7 unann4
8 unann5
9 unann6
10 unann7
11 unrev1
12 unrev2

Statistics: Mean 49.868; Variance 143.995; scale 0.346

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 3454 | 95.6 | 505 | 10 | A54101 | peroxisome prolifera | 0.00e+00 |
| 2 | 3439 | 95.2 | 475 | 10 | A49294 | peroxisome prolifera | 0.00e+00 |
| 3 | 3433 | 95.0 | 475 | 10 | S42489 | peroxisome prolifera | 0.00e+00 |
| 4 | 3311 | 91.6 | 470 | 10 | JN0881 | peroxisome prolifera | 0.00e+00 |
| 5 | 2579 | 71.4 | 477 | 9 | C42214 | peroxisome prolifera | 0.00e+00 |
| 6 | 1946 | 53.8 | 468 | 10 | A49289 | peroxisome prolifera | 3.90e-256 |



| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 7 | 1932 | 53.5 | 468 | 10 | S11659 | peroxisome prolifera | 4.42e-254 |
| 8 | 1932 | 53.5 | 468 | 10 | JC2085 | proliferator activat | 4.42e-254 |
| 9 | 1930 | 53.4 | 468 | 10 | A45288 | peroxisome prolifera | 8.69e-254 |
| 10 | 1919 | 53.1 | 441 | 10 | A45360 | steroid hormone rece | 3.58e-252 |
| 11 | 1894 | 52.4 | 474 | 9 | A42214 | peroxisome prolifera | 1.66e-248 |
| 12 | 1743 | 48.2 | 396 | 9 | B42214 | peroxisome prolifera | 2.22e-226 |
| 13 | 706 | 19.5 | 1237 | 9 | A34598 | ecdysone-induced pro | 8.84e-77 |
| 14 | 672 | 18.6 | 711 | 12 | S43464 | ecdysteroid-induced | 5.17e-72 |
| 15 | 641 | 17.7 | 1443 | 9 | S05979 | steroid hormone rece | 1.11e-67 |
| 16 | 528 | 14.6 | 1394 | 9 | B34598 | ecdysone-induced pro | 4.74e-52 |
| 17 | 525 | 14.5 | 373 | 6 | C36067 | thyroid hormone rece | 1.22e-51 |
| 18 | 518 | 14.3 | 369 | 3 | TVCHTB | thyroid hormone rece | 1.11e-50 |
| 19 | 517 | 14.3 | 410 | 12 | S14416 | thyroid hormone rece | 1.52e-50 |
| 20 | 517 | 14.3 | 398 | 6 | S23614 | thyroid hormone rece | 1.52e-50 |
| 21 | 516 | 14.3 | 410 | 6 | S26828 | thyroid hormone rece | 2.09e-50 |
| 22 | 516 | 14.3 | 410 | 6 | A40917 | thyroid hormone rece | 2.09e-50 |
| 23 | 516 | 14.3 | 410 | 3 | QRMSA1 | thyroid hormone rece | 2.09e-50 |
| 24 | 514 | 14.2 | 461 | 6 | A40377 | thyroid hormone rece | 3.92e-50 |
| 25 | 514 | 14.2 | 461 | 6 | A31820 | thyroid hormone rece | 3.92e-50 |
| 26 | 513 | 14.2 | 456 | 3 | TVHUAR | thyroid hormone rece | 5.37e-50 |
| 27 | 511 | 14.1 | 373 | 6 | D36067 | thyroid hormone rece | 1.01e-49 |
| 28 | 510 | 14.1 | 456 | 6 | A31116 | thyroid hormone rece | 1.38e-49 |
| 29 | 510 | 14.1 | 410 | 12 | S09178 | thyroid hormone rece | 1.38e-49 |
| 30 | 503 | 13.9 | 408 | 3 | TVCHVR | thyroid hormone rece | 1.25e-48 |
| 31 | 496 | 13.7 | 508 | 10 | A30226 | thyroid/steroid horm | 1.12e-47 |
| 32 | 491 | 13.6 | 410 | 6 | S06410 | thyroid hormone rece | 5.38e-47 |
| 33 | 490 | 13.6 | 614 | 10 | A32608 | thyroid hormone rece | 7.36e-47 |
| 34 | 488 | 13.5 | 418 | 3 | TVXLTA | thyroid hormone rece | 1.38e-46 |
| 35 | 485 | 13.4 | 65 | 10 | PN0676 | peroxisome prolifera | 3.52e-46 |
| 36 | 482 | 13.3 | 578 | 12 | S52913 | nuclear hormone rece | 9.01e-46 |
| 37 | 482 | 13.3 | 461 | 12 | JC4014 | steroid hormone-nucl | 9.01e-46 |
| 38 | 482 | 13.3 | 383 | 12 | S52909 | nuclear hormone rece | 9.01e-46 |
| 39 | 482 | 13.3 | 533 | 10 | JC2390 | nuclear receptor Rev | 9.01e-46 |
| 40 | 479 | 13.3 | 955 | 10 | C40045 | PML/retinoic acid re | 2.30e-45 |
| 41 | 477 | 13.2 | 459 | 6 | A41977 | retinoic acid recept | 4.30e-45 |
| 42 | 475 | 13.1 | 418 | 6 | B36067 | thyroid hormone rece | 8.03e-45 |
| 43 | 474 | 13.1 | 387 | 6 | S35744 | transforming protein | 1.10e-44 |
| 44 | 472 | 13.1 | 797 | 10 | B40044 | PML-1/retinoic acid | 2.05e-44 |
| 45 | 471 | 13.0 | 398 | 3 | TVFVVR | transforming protein | 2.80e-44 |

ALIGNMENTS

RESULT 1
ENTRY A54101 #type complete
TITLE peroxisome proliferator-activated receptor gamma-2 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 02-Aug-1994
ACCESSIONS A54101
REFERENCE A54101
#authors Tontonoz, P.; Hu, E.; Graves, R.A.; Budavari, A.I.; Spiegelman, B.M.
#journal Genes Dev. (1994) 8:1224-1234
#title mPPARgamma2: tissue-specific regulator of an adipocyte enhancer.
#accession A54101
##status preliminary
##molecule_type mRNA
##residues 1-505 ##label TON
##cross-references EMBL:U09138
KEYWORDS receptor
SUMMARY #length 505 #molecular-weight 57598 #checksum 3454

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  DB 10;  Score    3454;  Match 97.3%;  QryMatch 95.6%;  Pred. No. 0.00e+00;
  Matches   469;  Conservative   11;  Mismatches   2;  Indels   0;  Gaps   0;

Db     24 stsqeitmvdtempfwptnfgissvdlsvmedhshsfdikpfttvdfssisaphyedipf 83
          |: |:||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Qy     13 SAFNEMTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPF 72

Db     84 tradpmvadykydlklqeyqsaikvepasppyysektqlynrpheepsnslmaiecrvcg 143
          ||:||:|||||||||||||||||||||||||||||||||||||:||||||||||||||||
Qy     73 TRTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCG 132

Db    144 dkasgfhygvhacegckgffrrtirlkliydrcdlncrihkksrnkcqycrfqkclavgm 203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    133 DKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGM 192

Db    204 shnairfgrmpqaekekllaeissdidqlnpesadlralakhlydsyiksfpltkakara 263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    193 SHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARA 252

Db    264 iltgkttdkspfviydmnslmmgedkikfkhitplqeqskevairifqgcqfrsveavqe 323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    253 ILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQE 312

Db    324 iteyaknipgfinldlndqvtllkygvheiiytmlaslmnkdgvliseggqgfmtreflkn 383
          ||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||||:
Qy    313 ITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKS 372

Db    384 lrkpfgdfmepkfefavkfnalelddsdlaifiaviilsgdrpgllnvkpiediqdnllq 443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    373 LRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQ 432

Db    444 alelqlklnhpessqlfakvlqkmtdlrqivtehvqllqvikktetdmslhpllqeiykd 503
          ||||||||||||||||||:||||||||||||||||:||||||||||||||||||||||||
Qy    433 ALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKD 492

Db    504 ly 505
          ||
Qy    493 LY 494


RESULT    2
ENTRY             A49294      #type complete
TITLE             peroxisome proliferator-activated receptor gamma - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              19-May-1995 #sequence_revision 19-May-1995 #text_change
                    19-May-1995
ACCESSIONS        A49294
REFERENCE         A49294
   #authors       Zhu, Y.; Alvares, K.; Huang, Q.; Rao, M.S.; Reddy, J.K.
   #journal       J. Biol. Chem. (1993) 268:26817-26820
   #title         Cloning of a new member of the peroxisome
                    proliferator-activated receptor gene family from mouse
                    liver.
   #accession     A49294
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-475 ##label ZHU
      ##cross-references GB:U01841
SUMMARY           #length 475  #molecular-weight 54511  #checksum 6045

  DB 10;  Score    3439;  Match 98.1%;  QryMatch 95.2%;  Pred. No. 0.00e+00;
  Matches   466;  Conservative    9;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 mvdtempfwptnfgissvdlsvmedhshsfdikpfttvdfssisaphyedipftradpmv 60
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```
          ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||:||:|
Qy     20 MVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDPVV 79

Db     61 adykydlklqeyqsaikvepasppyysektqlynrpheepsnslmaiecrvcgdkasgfh 120
          ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Qy     80 ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGDKASGFH 139

Db    121 ygvhacegckgffrrtirlkliydrcdlncrihkksrnkcqycrfqkclavgmshnairf 180
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Qy    140 YGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRF 199

Db    181 grmpqaekekllaeissdidqlnpesadlralakhlydsyiksfpltkakarailtgktt 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    200 GRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTT 259

Db    241 dkspfviydmnslmmgedkikfkhitplqeqskevairifqgcqfrsveavqeiteyakn 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Qy    260 DKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKS 319

Db    301 ipgfinldlndqvtllkygvheiiytmlaslmnkdgvlisegqgfmtreflknlrkpfgd 360
          ||||:||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Qy    320 IPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGD 379

Db    361 fmepkfefavkfnalelddsdlaifiaviilsgdrpgllnvkpiediqdnllqalelqlk 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    380 FMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLK 439

Db    421 lnhpessqlfakvlqkmtdlrqivtehvqllhvikktetdmslhpllqeiykdly 475
          ||||||||||:||||||||||||||||:||||||||||||||||||||||||||||||
Qy    440 LNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 494


RESULT    3
ENTRY             S42489      #type complete
TITLE             peroxisome proliferator activated receptor - human
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                    06-Jan-1995
ACCESSIONS        S42489
REFERENCE         S42489
   #authors       Aperlo, C.; Pognonec, P.; Auwerx, J.; Boulukos, K.
   #submission    submitted to the EMBL Data Library, March 1994
   #description   Isolation and characterization of the human peroxisome
                    proliferator activated receptor, hPPARg, a member of the
                    nuclear hormone receptor superfamily.
   #accession     S42489
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-475 ##label APE
      ##cross-references EMBL:Z30972
SUMMARY           #length 475  #molecular-weight 54472  #checksum 5251

  DB 10;  Score    3433;  Match 97.7%;  QryMatch 95.0%;  Pred. No. 0.00e+00;
  Matches   464;  Conservative   11;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 mvdtempfwptnfgissvdlsmmddhshsfdikpfttvdfssisaphyedipftradpmv 60
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Db     61 adykydlklqeyqsaikvepasppyysekaqlynrpheepsnslmaiecrvcgdkasgfh 120
          ||||||||||||||||||||||||||||:||||:||||||||||||||||||||||||||
Qy     80 ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGDKASGFH 139

Db    121 ygvhacegckgffrrtirlkliydrcdlncrihkksrnkcqycrfqkclavgmshnairf 180
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     140 YGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRF 199

Db     181 grmpqaekekllaeissdidqlnpesadlralakhlydsyiksfpltkakarailtgktt 240
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Qy     200 GRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTT 259

Db     241 dkspfviydmnslmmgedkikfkhitplqeqskevairifqqgcqfrsveavqeiteyakn 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Qy     260 DKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKS 319

Db     301 ipgfinldlndqvtllkygvheiiytmlaslmnkdgvlisegqgfmtreflkslrkpfgd 360
                 ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     320 IPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGD 379

Db     361 fmepkfefavkfnalelddsdlaifiaviilsgdrpgllnvkpiediqdnllqalelqlk 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     380 FMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLK 439

Db     421 lnhpessqlfakvlqkmtdlrqivtehvqllhvikktetdmslhpllqeiykdly 475
                 ||||||||||||:||||||||||||||||||:||||||||||||||||||||||||
Qy     440 LNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 494


RESULT    4
ENTRY             JN0881     #type complete
TITLE             peroxisome proliferator activated receptor gamma precursor -
                    mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change
                    03-Mar-1995
ACCESSIONS        JN0881
REFERENCE         JN0881
   #authors       Chen, F.; Law, S.W.; O'Malley, B.W.
   #journal       Biochem. Biophys. Res. Commun. (1993) 196:671-677
   #title         Identification of two mPPAR related receptors and evidence
                    for the existence of five subfamily members.
   #accession     JN0881
      ##molecule_type mRNA
      ##residues       1-470 ##label CHE
      ##experimental_source heart
CLASSIFICATION    #superfamily erbA transforming protein homology
KEYWORDS          DNA binding
FEATURE
   1-22                #domain signal sequence #status predicted #label SIG\
   23-470              #product peroxisome proliferator activated receptor
                         gamma #status predicted #label MAT\
   107-393             #domain erbA transforming protein homology #label ERBA\
   130-194             #region DNA-binding
SUMMARY           #length 470  #molecular-weight 54014  #checksum 9480

  DB 10;  Score    3311;  Match 96.2%;  QryMatch 91.6%;  Pred. No. 0.00e+00;
  Matches   457;  Conservative   11;  Mismatches   2;  Indels   5;  Gaps   1;

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Qy      20 MVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDPVV 79

Db      61 adykydlklqeyqsaikvepasppyysektqlynrpheepsnslmaiecrvcgdkasgfh 120
           ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Qy      80 ADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGDKASGFH 139

Db     121 ygvhacegckgffrrtirlkliydrcdlncrihkksrnkcqycrfqkclavgmshnairf 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     140 YGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRF 199

Db     181 grdrqaekekllaeissdidqlnpesadlralakhlydsyiksfpltkakarailtgktt 240
           ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     200 GRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTT 259

Db     241 dkspfviydmssfmmgedkikfkhitplqeqskevairifqqgcqfrsveavqeiteyakn 300
           ||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||:
Qy     260 DKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKS 319

Db     301 ipgfinldlndqvtllkygvheiiytmlaslmnkdgvlisegqgfmtreflkslrkpfgd 360
           ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     320 IPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGD 379

Db     361 fmepkfefavkfnalelddsdlaifiaviilsgdrpgllnvkpiediqdnllq-----lk 415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||     ||
Qy     380 FMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLK 439

Db     416 lnhpessqlfakvlqkmtdlrqivtehvqllhvikktetdmslhplfqeiykdly 470
           ||||||||||:||||||||||||||||||:||||||||||||||:||||||||
Qy     440 LNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY 494


RESULT    5
ENTRY             C42214     #type complete
TITLE             peroxisome proliferator-activated receptor gamma,
                    xPPARgamma=nuclear hormone receptor - African clawed frog
ORGANISM          #formal_name Xenopus laevis #common_name African clawed frog
DATE              04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
                    18-Nov-1994
ACCESSIONS        C42214
REFERENCE         A42214
   #authors       Dreyer, C.; Krey, G.; Keller, H.; Givel, F.; Helftenbein, G.;
                    Wahli, W.
   #journal       Cell (1992) 68:879-887
   #title         Control of the peroxisomal beta-oxidation pathway by a novel
                    family of nuclear hormone receptors.
   #cross-references MUID:92191267
   #accession     C42214
      ##status        preliminary; not compared with conceptual translation
      ##molecule_type nucleic acid
      ##residues       1-477 ##label DRE
      ##cross-references NCBIP:88295
      ##note          sequence extracted from NCBI backbone
SUMMARY           #length 477  #molecular-weight 54055  #checksum 6850

  DB  9;  Score    2579;  Match 73.9%;  QryMatch 71.4%;  Pred. No. 0.00e+00;
  Matches   357;  Conservative   62;  Mismatches   50;  Indels   14;  Gaps   10;

Db       1 mvdtempfwsnlnfgmnsmdmsaledhcqpydikpfttvdfssins-hyddildektflc 59
           |||||||||:  |||::|:|:| :||| :::||||||||||||||:: ||:||     |
Qy      20 MVDTEMPFWPT-NFGISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDI----PFT- 73

Db      60 rndqspidykydlklqecqssikleppsppyfsdkpq-cskafedtpnsfiaiecrvcgd 118
           | |    |||||||||| ||:||:||:||||:|:| |  :|: |: :||::|||||||||
Qy      74 RTDPVVADYKYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGD 133

Db     119 kasgfhygvhacegckgffrrtirlkliyercdlncrihkksrnkcqfcrfqkclavgms 178
           ||||||||||||||||||||||||||||:|||||||||||||||:||||||||||||
Qy     134 KASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCRFQKCLAVGMS 193

Db     179 hnairfgrmpqaekekllaeissdidqlnpesadqrvlakhlydsyvksfpltkakapgh 238
           |||||||||||||||||||||||||||||||| | |||||||||:|||||||||| :
Qy     194 HNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAI 253
```

```
Db    239 pdgqshrqnsrgytrheladdgggsdqgavre-praeqgggdsnlpal-svalrg--gvr 294
          | :  ::|  :   ::     | |    :     :: : :  :  : :  :|:  :|:
Qy    254 LTGKT-TDKSP-FVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQ 311

Db    295 eitefaknipgfvsldlndqvtllkygvheiiftmlaslmnkdgvlvaeqqgfmtreflk 354
          ||||:||:||||||:||||||||||||||||||:|||||||||||||::|||||||||||
Qy    312 EITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLK 371

Db    355 slrkpfsdfmepkfefairfnslelddsdlaifvaviilsgdrpgllnvkpiediqdsll 414
          ||||||:|||||||||||::||:||||||||||:|||||||||||||||||||||||:||
Qy    372 SLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLL 431

Db    415 qalelqlklnhpdsaqlfakllqkmtdlrqvvtehvqllqlikkteadmclhpllqeiyk 474
          ||||||||||||:|:|||||||||||||||:|||||||:|||||:|| ||||||||||
Qy    432 QALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYK 491

Db    475 dly 477
          |||
Qy    492 DLY 494


RESULT    6
ENTRY           A49289     #type complete
TITLE           peroxisome proliferator-activated receptor - human
ORGANISM        #formal_name Homo sapiens #common_name man
DATE            07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
                  07-Apr-1994
ACCESSIONS      A49289
REFERENCE       A49289
   #authors     Sher, T.; Yi, H.F.; McBride, O.W.; Gonzalez, F.J.
   #journal     Biochemistry (1993) 32:5598-5604
   #title       cDNA cloning, chromosomal mapping, and functional
                  characterization of the human peroxisome proliferator
                  activated receptor.
   #accession   A49289
      ##status       preliminary
      ##molecule_type mRNA
      ##residues     1-468 ##label SHE
      ##cross-references GB:L02932
      ##note         authors translated the codon AAC for residue 33 as Asp
GENETICS
   #map_position 22
SUMMARY         #length 468  #molecular-weight 52267  #checksum 6622

  DB 10;  Score    1946;  Match 65.2%;  QryMatch 53.8%;  Pred. No. 3.90e-256;
  Matches   247;  Conservative   78;  Mismatches  51;  Indels   3;  Gaps   3;

Db     92 espsgal-niecricgdkasgyhygvhacegckgffrrtirlklvydkcdrsckiqkknr 150
          | || :|  ||||:|||||||:|||||||||||||||||||||:||:|| :|:|:||:|
Qy    117 EEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSR 176

Db    151 nkcqycrfhkclsvgmshnairfgrmprsekaklkaeiltcehdiedsetadlkslakri 210
          ||||||||:|||:|||||||||||||::|| || ||| : : |  ::|:|||::|||::
Qy    177 NKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHL 235

Db    211 yeaylknfnmnkvkarvilsgkasnnppfvihdmetlcmaektlvaklvan-giqnkeve 269
          |::|:|:| : | ||| ||:||:::::|||| ||::| |:|  :  | ::    |:|||
Qy    236 YDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVA 295

Db    270 vrifhccqctsvetvteltefakaipafanldlndqvtllkygvyeaifamlssvmnkdg 329
          :|||: ||  |||:| |:||:||:||:| ||||||||||||||| | |::||:|:|||||
Qy    296 IRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDG 355
```



```
Db    330 mlvaygngfitreflkslrkpfcdimepkfdfamkfnalelddsdislfvaaiiccgdrp 389
          :|:: | ||:|||||||||||| |:|||||:||:|||||||||||:::|:| ||  ||||
Qy    356 VLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRP 415

Db    390 gllnvghiekmqegivhvlrlhlqsnhpddiflfpkllqkmadlrqlvtehaqlvqiikk 449
          |||||  || :|: ::: | |:|  |||:   ||:||||||:||||:|||| ||:|:|||
Qy    416 GLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKK 475

Db    450 tesdaalhpllqeiyrdmy 468
          ||:| :|||||||||:|:|
Qy    476 TETDMSLHPLLQEIYKDLY 494


RESULT    7
ENTRY           S11659     #type complete
TITLE           peroxisome proliferator-activated receptor - mouse
ORGANISM        #formal_name Mus musculus #common_name house mouse
DATE            13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                  13-Jan-1995
ACCESSIONS      S11659
REFERENCE       S11659
   #authors     Issemann, I.; Green, S.
   #journal     Nature (1990) 347:645-650
   #title       Activation of a member of the steroid hormone receptor
                  superfamily by peroxisome proliferators.
   #cross-references MUID:91015382
   #accession   S11659
      ##status       preliminary
      ##molecule_type mRNA
      ##residues     1-468 ##label ISS
SUMMARY         #length 468  #molecular-weight 52432  #checksum 4196

  DB 10;  Score    1932;  Match 64.6%;  QryMatch 53.5%;  Pred. No. 4.42e-254;
  Matches   245;  Conservative   79;  Mismatches  53;  Indels   2;  Gaps   2;

Db     91 despgsalniecricgdkasgyhygvhacegckgffrrtirlklvydkcdrsckiqkknr 150
          :|:: | : ||||:|||||||:|||||||||||||||||||||:||:|| :|:|:||:|
Qy    117 EEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSR 176

Db    151 nkcqycrfhkclsvgmshnairfgrmprsekaklkaeiltcehdlkdsetadlkslqkri 210
          ||||||||:|||:|||||||||||||::|| || ||| : : |  ::|:|||::|:|::
Qy    177 NKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHL 235

Db    211 heaylknfnmnkvkarvilagktsnnppfvihdmetlcmaektlvakmvangved-keae 269
           ::|:|:| : | ||| ||:|||::::|||| ||::| |:|  :  | ::   |: ||
Qy    236 YDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVA 295

Db    270 vrffhccqcmsvetvteltefakaipgfanldlndqvtllkygvyeaiftmlsslmnkdg 329
          :|:|: ||  |||:| |:||:||:|||| |||||||||||||| | |:|||:|||||||
Qy    296 IRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDG 355

Db    330 mliaygngfitreflknlrkpfcdimepkfdfamkfnalelddsdislfvaaiiccgdrp 389
          :||: | ||:||||||:||||| |:|||||:||:|||||||||||:::|:| ||  ||||
Qy    356 VLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRP 415

Db    390 gllnigyieklqegivhvlklhlqsnhpddtflfpkllqkmvdlrqlvtehaqlvqvikk 449
          ||||:  || :|: ::: | |:|  |||: : ||:|||||| ||||:|||| ||:|||||
Qy    416 GLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKK 475

Db    450 tesdaalhpllqeiyrdmy 468
          ||:| :|||||||||:|:|
Qy    476 TETDMSLHPLLQEIYKDLY 494
```

```
RESULT    8
ENTRY             JC2085      #type complete
TITLE             proliferator activated receptor alpha chain - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change
                    14-Jul-1994
ACCESSIONS        JC2085
REFERENCE         JC2085
   #authors       Gearing, K.L.; Crickmore, A.; Gustafsson, J.A.
   #journal       Biochem. Biophys. Res. Commun. (1994) 199:255-263
   #title         Structure of the mouse peroxisome proliferator activated
                    receptor alpha gene.
   #accession     JC2085
      ##molecule_type DNA
      ##residues       1-468 ##label GEA
      ##cross-references EMBL:X75287; EMBL:X75288; EMBL:X75289; EMBL:X75290;
                        EMBL:X75291; EMBL:X75292; EMBL:X75293
COMMENT     This protein mediates transcription of responsive genes which
              include those encoding peroxisomal enzymes and members of the
              cytochrome P450 family of drug metabolising enzymes.
GENETICS
   #gene          PPARalpha
   #introns       70/1; 123/2; 170/1; 237/3; 387/1
KEYWORDS          DNA binding; receptor; zinc finger
SUMMARY           #length 468  #molecular-weight 52347  #checksum 3890

  DB 10;  Score    1932;  Match 64.6%;  QryMatch 53.5%;  Pred. No. 4.42e-254;
  Matches   245;  Conservative   79;  Mismatches  53;  Indels   2;  Gaps   2;

Db     91 despgsalniecricgdkasgyhygvhacegckgffrrtirlklvydkcdrsckiqkknr 150
          :|:: | : ||||:|||||||:|||||||||||||||||||||||:||:|| :|:|:||:|
Qy    117 EEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSR 176

Db    151 nkcqycrfhkclsvgmshnairfgrmprsekaklkaeiltcehdlkdsetadlkslqkri 210
          |||||||||:|||:|||||||||||||||::|| || ||| : : |  ::|:|||::|:|:: 
Qy    177 NKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHL 235

Db    211 heaylknfnmnkvkarvilagktsnnppfvihdmetlcmaektlvakmvangved-keae 269
           ::|:|:| : | ||| ||:|||::::|||| ||::| |:|  :  | ::   |: ||
Qy    236 YDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVA 295

Db    270 vrffhccqcmsvetvteltefakaipgfanldlndqvtllkygvyeaiftmlsslmnkdg 329
          :|:|: ||  |||:| |:||:||:|||| ||||||||||||||| | |:|||:|||||||
Qy    296 IRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDG 355

Db    330 mliaygngfitreflknlrkpfcdimepkfdfamkfnalelddsdislfvaaiiccgdrp 389
          :||: | ||:|||||:|||| |:|||||:||:|||||||||:::|:| ||  ||||
Qy    356 VLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRP 415

Db    390 gllnigyieklqegivhvlklhlqsnhpddtflfpkllqkmvdlrqlvtehaqlvqvikk 449
          ||||:  || :|: ::: | |:|  |||: : ||:|||||| ||||:|||| ||:|||||
Qy    416 GLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKK 475

Db    450 tesdaalhpllqeiyrdmy 468
          ||:| :||||||||:|:|
Qy    476 TETDMSLHPLLQEIYKDLY 494


RESULT    9
ENTRY             A45288      #type complete
TITLE             peroxisome proliferator-activated receptor - rat
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
                    27-Jun-1994
```



```
ACCESSIONS        A45288
REFERENCE         A45288
   #authors       Goettlicher, M.; Widmark, E.; Li, Q.; Gustafsson, J.A.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4653-4657
   #title         Fatty acids activate a chimera of the clofibric
                    acid-activated receptor and the glucocorticoid receptor.
   #accession     A45288
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-468 ##label GOE
      ##cross-references GB:M88592
SUMMARY           #length 468  #molecular-weight 52377  #checksum 4509

  DB 10;  Score    1930;  Match 65.2%;  QryMatch 53.4%;  Pred. No. 8.69e-254;
  Matches   247;  Conservative   76;  Mismatches  53;  Indels   3;  Gaps   3;

Db     92 espgnal-niecricgdkasgyhygvhacegckgffrrtirlklaydkcdrsckiqkknr 150
          | |:|:|  ||||:|||||||:|||||||||||||||||||||| ||:|| :|:|:||:|
Qy    117 EEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSR 176

Db    151 nkcqycrfhkclsvgmshnairfgrmprsekaklkaeiltcehdlkdsetadlkslakri 210
          ||||||||:|||:|||||||||||||::|| || ||| : : |  ::|:|||::|||:: 
Qy    177 NKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAKHL 235

Db    211 heaylknfnmnkvkarvilagktsnnppfvihdmetlcmaektlvakmvan-gvenkeae 269
           ::|:|:| : | ||| ||:|||::::|||| ||::| |:|  :  | ::    ::||
Qy    236 YDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVA 295

Db    270 vrffhccqcmsvetvteltefakaipgfanldlndqvtllkygvyeaiftmlsslmnkdg 329
          :|:|: ||  |||:| |:||:||:|||| ||||||||||||||| | |:|||:|||||||
Qy    296 IRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDG 355

Db    330 mliaygngfitreflknlrkpfcdimepkfdfamkfnalelddsdislfvaaiiccgdrp 389
          :||: | ||:|||||:|||| |:|||||:||:|||||||||:::|:| ||  ||||
Qy    356 VLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRP 415

Db    390 gllnigyieklqegivhvlklhlqsnhpddtflfpkllqkmvdlrqlvtehaqlvqvikk 449
          ||||:  || :|: ::: | |:|  |||: : ||:|||||| ||||:|||| ||:|||||
Qy    416 GLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKK 475

Db    450 tesdaalhpllqeiyrdmy 468
          ||:| :||||||||:|:|
Qy    476 TETDMSLHPLLQEIYKDLY 494


RESULT   10
ENTRY             A45360      #type complete
TITLE             steroid hormone receptor NUC1 - human
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
                    11-Apr-1995
ACCESSIONS        A45360
REFERENCE         A45360
   #authors       Schmidt, A.; Endo, N.; Rutledge, S.J.; Vogel, R.; Shinar, D.;
                    Rodan, G.A.
   #journal       Mol. Endocrinol. (1992) 6:1634-1641
   #title         Identification of a new member of the steroid hormone
                    receptor superfamily that is activated by a peroxisome
                    proliferator and fatty acids.
   #cross-references MUID:93078797
   #accession     A45360
      ##status        preliminary; not compared with conceptual translation
      ##molecule_type nucleic acid
      ##residues      1-441 ##label SCH
```

```
      ##cross-references NCBIP:118801
      ##experimental_source osteosarcoma SAOS-2/B10 cells
      ##note          sequence extracted from NCBI backbone
SUMMARY          #length 441  #molecular-weight 49929  #checksum 7063

  DB 10;  Score    1919;  Match 65.6%;  QryMatch 53.1%;  Pred. No. 3.58e-252;
  Matches   244;  Conservative   78;  Mismatches  49;  Indels   1;  Gaps   1;

Db     70 lnmecrvcgdkasgfhygvhacegckgffrrtirmkleyekcersckiqkknrnkcqycr 129
          : :|||||||||||||||||||||||||||||||||:|| |::|: :|:|:||:|||||||||
Qy    124 MAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCR 183

Db    130 fqkclalqmshnairfgrmpeaekrklvagltanegsqynpqvadlkafskhiynaylkn 189
          |||||:|||||||||||||:||| ||:| ::::   | ||: |||:|::||:|::|:|:
Qy    184 FQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDID-QLNPESADLRALAKHLYDSYIKS 242

Db    190 fnmtkkkarsiltgkashtapfvihdietlwqaekglvwkqlvnglppykeisvhvfyrc 249
          | :|| |||:|||||::  :|||| |:::|  :|  :  |::       ||:::::|  |
Qy    243 FPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGC 302

Db    250 qcttvetvreltefaksipsfsslflndqvtllkygvheaifpmlasivnkdgllvangs 309
          |  :||:|:|:||:|||||:| :| ||||||||||||| |: ||||::||||:|:::|
Qy    303 QFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQ 362

Db    310 gfvtreflrslrkpfsdiiepkfefavkfnalelddsdlalfiaaiilcqdrpglmnvpr 369
          ||:|||||:||||||:|::|||||||||||||||||||:||| ||| ||||||:||
Qy    363 GFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKP 422

Db    370 veaiqdtilralefhlqanhpdaqylfpkllqkmadlrqlvtehaqmmqrikktetetsl 429
          :| ||| :|:|||::|  |||::  ||:||||||:||||:|||| |::| ||||||: ||
Qy    423 IEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSL 482

Db    430 hpllqeiykdmy 441
          ||||||||||:|
Qy    483 HPLLQEIYKDLY 494


RESULT   11
ENTRY            A42214     #type complete
TITLE            peroxisome proliferator-activated receptor alpha,
                   xPPARalpha=nuclear hormone receptor - African clawed frog
ORGANISM         #formal_name Xenopus laevis #common_name African clawed frog
DATE             04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
                   18-Nov-1994
ACCESSIONS       A42214
REFERENCE        A42214
   #authors      Dreyer, C.; Krey, G.; Keller, H.; Givel, F.; Helftenbein, G.;
                   Wahli, W.
   #journal      Cell (1992) 68:879-887
   #title        Control of the peroxisomal beta-oxidation pathway by a novel
                   family of nuclear hormone receptors.
   #cross-references MUID:92191267
   #accession    A42214
      ##status        preliminary; not compared with conceptual translation
      ##molecule_type nucleic acid
      ##residues      1-474 ##label DRE
      ##cross-references NCBIP:88292
      ##note          sequence extracted from NCBI backbone
SUMMARY          #length 474  #molecular-weight 52855  #checksum 8486

  DB  9;  Score    1894;  Match 64.8%;  QryMatch 52.4%;  Pred. No. 1.66e-248;
  Matches   247;  Conservative   74;  Mismatches  56;  Indels   4;  Gaps   4;

Db     97 aedaacksl-nlecrvcsdkasgfhygvhacegckgffrrtirlklvydrcermckiqkk 155
```



```
          : : : :||  :|||||:|||||||||||||||||||||||||||||||:||||:  |:|:||
Qy    115 PHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKK 174

Db    156 nrnkcqycrfekclnvgmshnairfgrmprsekaklkaevlmcdqdvkdsqmadllslar 215
          :|||||||||:||| |||||||||||||::|| || ||:   | |  ::: ||| :||:
Qy    175 SRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEI-SSDIDQLNPESADLRALAK 233

Db    216 liydaylknfnmnkvkarailtgkasn-ppfvihdmetlcmaektlvaklvan-giqnke 273
          :||:|:|:| : | ||||||||:: :|||| ||::| |:|  :  | ::   |:||
Qy    234 HLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKE 293

Db    274 aevrifhccqctsvetvteltefaksipgfteldlndqvtllkygvyeamfamlasvmnk 333
            :|||: ||  |||:| |:||:|||||| :|||||||||||| | :::||||:|||
Qy    294 VAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNK 353

Db    334 dgmlvaygngfitreflkslrkpigdmmepkfefamkfnalelddsdlslfvaaliccgd 393
          ||:|:: | ||:|||||||||:|| ||||||||:|||||||||||::|:| :|  ||
Qy    354 DGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGD 413

Db    394 rpglvnipsiekmqesivhvlklhlqsnhpddsflfpkllqkmadlrqlvtehaqlvqti 453
          ||||:|: :|| :|:::::| |:|  |||: | ||:||||||:||||:|||| ||:| |
Qy    414 RPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVI 473

Db    454 kktetdaalhpllqeiyrdmy 474
          |||||| :||||||||:|:|
Qy    474 KKTETDMSLHPLLQEIYKDLY 494


RESULT   12
ENTRY            B42214     #type complete
TITLE            peroxisome proliferator-activated receptor beta,
                   xPPARbeta=nuclear hormone receptor - African clawed frog
ORGANISM         #formal_name Xenopus laevis #common_name African clawed frog
DATE             04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
                   18-Nov-1994
ACCESSIONS       B42214
REFERENCE        A42214
   #authors      Dreyer, C.; Krey, G.; Keller, H.; Givel, F.; Helftenbein, G.;
                   Wahli, W.
   #journal      Cell (1992) 68:879-887
   #title        Control of the peroxisomal beta-oxidation pathway by a novel
                   family of nuclear hormone receptors.
   #cross-references MUID:92191267
   #accession    B42214
      ##status        preliminary; not compared with conceptual translation
      ##molecule_type nucleic acid
      ##residues      1-396 ##label DRE
      ##cross-references NCBIP:88294
      ##note          sequence extracted from NCBI backbone
SUMMARY          #length 396  #molecular-weight 44991  #checksum 4744

  DB  9;  Score    1743;  Match 57.9%;  QryMatch 48.2%;  Pred. No. 2.22e-226;
  Matches   221;  Conservative   79;  Mismatches  80;  Indels   2;  Gaps   2;

Db     17 stplehqets-qsvdckicgdrasgfhygvhacegckgffrrtirmrlqyehcdrnckiq 75
          : | |    |  :::|::|||:|||||||||||||||||||||||::| |::|| ||:|:
Qy    113 NKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIH 172

Db     76 kknrnkcqycrfnkclslgmshnairfgrmpesekrklvqapvsdsaapdspvsdldvls 135
          ||:|||||||| |||::|||||||||||||::|| ||:   ||   ::  :||  |:
Qy    173 KKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALA 232

Db    136 qlihssymntftmtkkrardiltgrns-ispfvihdmdtlwqaeqgtvweqlptqnltgt 194
            :  ||:::| :|| :|| |||||: :  ||||| ||::|  :|:    ::      :
```

```
Qy    233 KHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSK 292

Db    195 eigvhvfyrcqctsvetvralтdfakripgfgtlylndqvtllkygvheaifcmlaslmn 254
          |:::::|  ||  |||:|: :|::|| ||||  | ||||||||||||| |: |||||||
Qy    293 EVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMN 352

Db    255 kdgllvaggrgfvtreflrslrqpfchimepkfhfaskfnalelndsdlalfvasiilcg 314
          |||:|:: |:||:|||||:||| ||  :|||| || |||||||:|||||:|:| ||| |
Qy    353 KDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSG 412

Db    315 drpglinpsqvediqegilgalrrhlkashtdapflfpkllhkmadlrqlvtehaelvqs 374
          |||||:|   :||||: :| ||  :|| :| ::: ||:|||:||:||||:|||| :|:|
Qy    413 DRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQV 472

Db    375 ikrtessaalhpllqeiyrdmy 396
          ||:||:  :|||||||||:|:|
Qy    473 IKKTETDMSLHPLLQEIYKDLY 494


RESULT   13
ENTRY            A34598     #type complete
TITLE            ecdysone-induced protein E75A - fruit fly (Drosophila
                   melanogaster)
ORGANISM         #formal_name Drosophila melanogaster
DATE             29-Jun-1990 #sequence_revision 29-Jun-1990 #text_change
                   15-Oct-1994
ACCESSIONS       A34598
REFERENCE        A34598
   #authors      Segraves, W.A.; Hogness, D.S.
   #journal      Genes Dev. (1990) 4:204-219
   #title        The E75 ecdysone-inducible gene responsible for the 75B early
                   puff in Drosophila encodes two new members of the steroid
                   receptor superfamily.
   #cross-references MUID:90249727
   #accession    A34598
      ##status       preliminary
      ##molecule_type DNA
      ##residues     1-1237 ##label SEG
      ##cross-references GB:X51548
CLASSIFICATION   #superfamily erbA transforming protein homology
KEYWORDS         alternative splicing; DNA binding; zinc finger
FEATURE
   243-520           #domain erbA transforming protein homology #label ERBA
SUMMARY          #length 1237  #molecular-weight 133330  #checksum 6126

  DB  9;  Score     706;  Match 34.1%;  QryMatch 19.5%;  Pred. No. 8.84e-77;
  Matches   123;  Conservative   92;  Mismatches 127;  Indels  19;  Gaps  17;

Db    242 tvlcrvcgdkasgfhygvhscegckgffrrsiqqkiqyrpctknqqcsilrinrnrcqyc 301
          :: |||||||||||||||||:|||||||||||:|: |: |  |  :  | | : :|||:||||
Qy    125 AIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRC--DLNCRIHKKSRNKCQYC 182

Db    302 rlkkciavgmsrdavrfgrvpkrekarilaamqqst-q-nr-gqq-ralatel-ddqprl 356
          |: ||:|||||::|:||||:|  || ::|| :     | |  : : |||| | |   :
Qy    183 RFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKS 242

Db    357 la-avlrahletceftkekvs-amrqrardcpsysmptl-lacplnpapelqseqef-s- 411
          :: :  :|:      | :| :  : :      :  :  :    ||   :   : : | :
Qy    243 FPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGC 302

Db    412 q-rfahvirgvidfagmipgfqlltqddkftllkaglfdalfvrlicmfdssinsiicln 470
          | |    :: : ::|  |||| |  :|  |||| |: : ::  |  : :     :|  :
Qy    303 QFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKD-GVLIS-E 360
```



```
Db    471 gqv-mrrdaiqnganarf--lvdstfnfaermnsmnltdaeiglfcaivlitpdrpglrn 527
          ||  | |: : ::    |  :::: |:|| : |:::| |:::::| |::::: ||||| |
Qy    361 GQGFMTRE-FLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLN 419

Db    528 leliekmysrlkgclqyivaqnrpdqpeflaklletmpdlrtlstlhteklvvfrtehke 587
          :  || :   |   |:  :  |:|: ::::||||: | ||| : | | : | |::    :
Qy    420 VKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETD 479

Db    588 l 588
          :
Qy    480 M 480


RESULT   14
ENTRY            S43464     #type complete
TITLE            ecdysteroid-induced E75 protein - Galleria mellonella
ORGANISM         #formal_name Galleria mellonella
DATE             23-Nov-1994 #sequence_revision 23-Nov-1994 #text_change
                   23-Nov-1994
ACCESSIONS       S43464
REFERENCE        S43464
   #authors      Jindra, M.; Sehnal, F.; Riddiford, L.M.
   #journal      Eur. J. Biochem. (1994) 221:665-675
   #title        Isolation, characterization and developmental expression of
                   the ecdysteroid-induced E75 gene of the wax moth Galleria
                   mellonella.
   #accession    S43464
      ##status       preliminary
      ##residues     1-711 ##label JIN
      ##cross-references GB:U02620
SUMMARY          #length 711  #molecular-weight 78529  #checksum 2665

  DB 12;  Score     672;  Match 33.4%;  QryMatch 18.6%;  Pred. No. 5.17e-72;
  Matches   121;  Conservative   92;  Mismatches 126;  Indels  23;  Gaps  20;

Db     44 tvlcrvcgdkasgfhygvhscegckgffrrsiqqkiqyrpctknqqcsilrinrnrcqyc 103
          :: |||||||||||||||||:||||||||||:|: |: |  |  :  | | : :||:||||
Qy    125 AIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRC--DLNCRIHKKSRNKCQYC 182

Db    104 rlkkciavgmsrdavrfgrvpkrekarilaamqsstrah-eqaa--a-a-elddg-pr- 156
          |: ||:|||||::|:||||:|  || ::|| : |   : : | |   | |  | |:  :
Qy    183 RFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKS 242

Db    157 l-larv-vrahldtceftrdr-va-amrngardcptysqptlacplnpapelqsekef-s 211
          : |::   || |      :   |   | :          :: ||   :   : : | :
Qy    243 FPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHIT-PLQEQSKEVAIRIFQG 301

Db    212 -q-rfahvirgvidfaglipgfqlltqddkftllksglfdalfvrlicmfdaplnsiicl 269
           | |    :: : ::|  |||| |  :|  |||| |: : ::  |  : :     :|
Qy    302 CQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKD-GVLIS- 359

Db    270 ngq-lmkrdsiqsganarf--lvdstfkfaermnsmnltdaeiglfcaivlitpdrpglr 326
          :|| :| |: : |  :: |  :::: | || : |:::| |:::::| |::::: |||||
Qy    360 EGQGFMTREFLKSLRKP-FGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLL 418

Db    327 nvelvermhsrlksclqtviaqnrsdgpgflrelmdtlpdlrtlstlhteklvvfrtehk 386
          ||  :| ::  |   |:  :  |:::::  ::  |:: : ||| : | | : | |::
Qy    419 NVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTET 478

Db    387 el 388
          ::
Qy    479 DM 480
```

```
RESULT   15
ENTRY            S05979     #type complete
TITLE            steroid hormone receptor homolog - fruit fly (Drosophila
                   melanogaster)
ALTERNATE_NAMES  puff 75B protein
ORGANISM         #formal_name Drosophila melanogaster
DATE             01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change
                   15-Oct-1994
ACCESSIONS       S05979
REFERENCE        S05979
   #authors      Feigl, G.; Gram, M.; Pongs, O.
   #journal      Nucleic Acids Res. (1989) 17:7167-7178
   #title        A member of the steroid hormone receptor gene family is
                   expressed in the 20-OH-ecdysone inducible puff 75B in
                   Drosophila melanogaster.
   #cross-references MUID:90016778
   #accession    S05979
      ##molecule_type mRNA
      ##residues      1-1443 ##label FEI
      ##cross-references EMBL:X15586
GENETICS
   #map_position 3 75B
CLASSIFICATION   #superfamily erbA transforming protein homology
KEYWORDS         alternative splicing; DNA binding; zinc finger
FEATURE
   452-727            #domain erbA transforming protein homology #label ERBA
SUMMARY          #length 1443  #molecular-weight 156264  #checksum 6391

  DB  9;  Score     641;  Match 34.2%;  QryMatch 17.7%;  Pred. No. 1.11e-67;
  Matches   124;  Conservative   88;  Mismatches 126;  Indels  25;  Gaps  23;

Db    451 tvlcrvcgdkasgfhygvhscegckgffrrsiqqkiqyrpctknqqcsilrinrnrcqyc 510
          :: ||||||||||||||||:|||||||||||:|: |: |  |  :  | | : :||:||||
Qy    125 AIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRC--DLNCRIHKKSRNKCQYC 182

Db    511 rlkkciavgmsrdavrfgrvpkrekariwrpcnra-priaa-ssd-psppswm-tshass 566
          |: ||:|||||::|:||||:|  || ::    :    :: : |:|  : :  :  |   |
Qy    183 RFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKS 242

Db    567 -ppccc-ah-letceft-kek-vs-amrh-grglpstpc-htsglsaepapelqseqef- 617
           |     |: : |   | |   |   |     |       | : |  | : |: : : |
Qy    243 FPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPL-QEQSKEV-AIRIFQ 300

Db    618 s-q-rfahvirgvidfagmipgfqlltqddkftllkaglfdalfvrlicmfdssinsiic 675
          : | |    :: : ::|  |||| |  :|  |||| |: : ::  |  : :     :|
Qy    301 GCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKD-GVLIS 359

Db    676 lngqv-mrrdaiqnganarf--lvdstfnfaermnsmnltdaeiglfcaivlitpdrpgl 732
           :||  | |: : ::    |  :::: |:|| : |:::| |::::::| |::::: |||||
Qy    360 -EGQGFMTRE-FLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGL 417

Db    733 rnleliekmysrlkgclqyivaqnrpdqpeflaklletmpdlrtlstlhteklvvfrteh 792
          |:  || :   |   |:  :  |:|: ::::|||||: | ||| : | | : | |::
Qy    418 LNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTE 477

Db    793 kel 795
          ::
Qy    478 TDM 480

Search completed: Fri Nov 17 08:31:34 1995
Job time : 24 secs.
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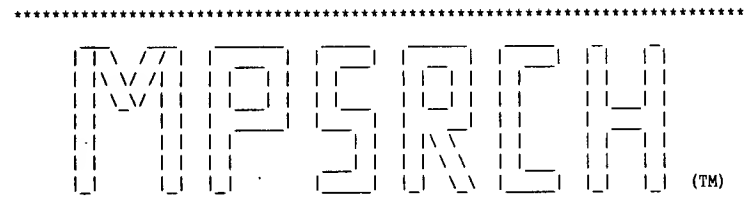


Release 2.1D John F. Collins, Biocomputing Research Unit.


MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Nov 17 08:31:51 1995; MasPar time 8.68 Seconds
361.722 Million cell updates/sec

Tabular output not generated.

Title: >US-08-380-051-2#
Description: (1:494) from US08380051.pep
Perfect Score: 3614
Sequence: 1 MLKLIVPFLKRESAFNEMTM.....KTETDMSLHPLLQEIYKDLY 494

Scoring table: PAM 150
Gap 11

Searched: 53402 seqs, 6354270 residues

Database: a_geneseq8
1 part1
2 part2
3 part3
4 part4
5 part5
6 part6
7 part7
8 part8
9 part9
10 part10

Statistics: Mean 36.352; Variance 186.140; scale 0.195

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 1921 | 53.2 | 441 | 8 | R41875 | Steroid hormone recep | 3.70e-146 |
| 2 | 1862 | 51.5 | 439 | 6 | R33745 | XR4. | 3.09e-141 |
| 3 | 680 | 18.8 | 1237 | 3 | R13791 | E75A protein. | 1.22e-43 |
| 4 | 512 | 14.2 | 456 | 2 | P80921 | Sequence encoded by h | 3.89e-30 |
| 5 | 510 | 14.1 | 410 | 2 | P80936 | Sequence encode by th | 5.61e-30 |
| 6 | 501 | 13.9 | 514 | 8 | R47621 | Rat thyroid hormone r | 2.92e-29 |
| 7 | 482 | 13.3 | 461 | 9 | R52980 | Human recombinant ste | 9.45e-28 |
| 8 | 472 | 13.1 | 797 | 5 | R27533 | myl/RAR-alpha fusion. | 5.87e-27 |



| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 9 | 471 | 13.0 | 440 | 6 | R33744 | XR2. | 7.05e-27 |
| 10 | 464 | 12.8 | 462 | 5 | R27534 | RAR-alpha protein. | 2.53e-26 |
| 11 | 463 | 12.8 | 462 | 2 | R10547 | Murine Retinoic Acid | 3.03e-26 |
| 12 | 462 | 12.8 | 462 | 1 | P90395 | Retinoic acid recepto | 3.64e-26 |
| 13 | 459 | 12.7 | 448 | 1 | P90341 | hap (hepatoma) protei | 6.29e-26 |
| 14 | 457 | 12.6 | 448 | 10 | R55128 | Retinoic acid recepto | 9.05e-26 |
| 15 | 456 | 12.6 | 448 | 2 | R10548 | Murine Retinoic Acid | 1.09e-25 |
| 16 | 455 | 12.6 | 458 | 3 | R20465 | Mouse retinoic acid r | 1.30e-25 |
| 17 | 455 | 12.6 | 454 | 2 | R10182 | Recombinant human gam | 1.30e-25 |
| 18 | 455 | 12.6 | 454 | 2 | R10550 | Human Retinoic Acid R | 1.30e-25 |
| 19 | 455 | 12.6 | 447 | 3 | R20466 | Mouse retinoic acid r | 1.30e-25 |
| 20 | 453 | 12.5 | 636 | 2 | R07683 | gag protein precursor | 1.87e-25 |
| 21 | 452 | 12.5 | 490 | 2 | P80926 | Sequence of the human | 2.25e-25 |
| 22 | 446 | 12.3 | 490 | 5 | R26899 | HerbA-T sequence. | 6.69e-25 |
| 23 | 444 | 12.3 | 458 | 2 | R10549 | Skin-specific murine | 9.63e-25 |
| 24 | 440 | 12.2 | 345 | 2 | P80922 | Sequence of the carbo | 1.99e-24 |
| 25 | 432 | 12.0 | 548 | 6 | R33741 | XR1. | 8.50e-24 |
| 26 | 411 | 11.4 | 487 | 3 | R13794 | Drosophila hormone re | 3.81e-22 |
| 27 | 385 | 10.7 | 483 | 3 | R12226 | Human TR2-5 androgen | 4.12e-20 |
| 28 | 385 | 10.7 | 463 | 3 | R13800 | Mouse RXR-gamma retin | 4.12e-20 |
| 29 | 385 | 10.7 | 467 | 3 | R12227 | Human TR2-9 DNA bindi | 4.12e-20 |
| 30 | 385 | 10.7 | 483 | 1 | P90998 | TR2-5 DNA clone. | 4.12e-20 |
| 31 | 385 | 10.7 | 603 | 3 | R12228 | Human TR2-11 DNA bind | 4.12e-20 |
| 32 | 385 | 10.7 | 463 | 7 | R39471 | mRXR-gamma. | 4.12e-20 |
| 33 | 382 | 10.6 | 533 | 7 | R39468 | hRXR-beta1. | 7.06e-20 |
| 34 | 382 | 10.6 | 446 | 2 | R11837 | H2RIIBP nuclear hormo | 7.06e-20 |
| 35 | 382 | 10.6 | 448 | 7 | R39467 | mRXR-beta. | 7.06e-20 |
| 36 | 381 | 10.5 | 151 | 10 | R55161 | Fragment of retinoic | 8.45e-20 |
| 37 | 381 | 10.5 | 418 | 1 | R07294 | Chicken ovalbumin ups | 8.45e-20 |
| 38 | 379 | 10.5 | 467 | 7 | R39470 | mRXR-alpha. | 1.21e-19 |
| 39 | 379 | 10.5 | 462 | 3 | R13798 | Human RXR-alpha retin | 1.21e-19 |
| 40 | 379 | 10.5 | 467 | 3 | R13799 | Mouse RXR-alpha retin | 1.21e-19 |
| 41 | 377 | 10.4 | 510 | 7 | R39469 | hRXR-beta2. | 1.73e-19 |
| 42 | 373 | 10.3 | 513 | 3 | R14304 | Insect steroid recept | 3.55e-19 |
| 43 | 373 | 10.3 | 513 | 8 | R48065 | D. melanogaster ultra | 3.55e-19 |
| 44 | 362 | 10.0 | 601 | 6 | R33747 | XR79. | 2.54e-18 |
| 45 | 359 | 9.9 | 184 | 3 | R12225 | Human TR2-7 DNA bindi | 4.34e-18 |

ALIGNMENTS

RESULT 1
ID R41875 standard; Protein; 441 AA.
AC R41875;
DT 13-APR-1994 (first entry)
DE Steroid hormone receptor (NUCI).
KW Steroid; hormone; receptor; osteosarcoma; superfamily.
OS Homo sapiens.
PN GB2265376-A.
PD 29-SEP-1993.
PF 23-MAR-1993; 006043.
PR 24-MAR-1992; US-857055.
PA (MERI ) MERCK & CO INC.
PI Rodan GA, Rutledge SJ, Schmidt A, Vogel RL;
DR WPI; 93-305586/39.
DR N-PDSB; Q48939.
PT New human steroid hormone receptor NUCI - used to assay and
PT evaluate ligands binding to the receptor
PS Claim 5; Page 39-40; 62pp; English.
CC The steroid hormone receptor (designated NUCI) is used in assays to
CC identify and evaluate chemical entities that bind to it.
SQ Sequence 441 AA;

DB 8; Score 1921; Match 65.6%; QryMatch 53.2%; Pred. No. 3.70e-146;

Matches 244; Conservative 79; Mismatches 48; Indels 1; Gaps 1;

```
Db     70 lnmecrvcgdkasgfhygvhacegckgffrrtirmkleyekcersckiqkknrnkcqycr 129
          : :|||||||||||||||||||||||||||||||||||||:|| |::|: :|:|:||:||||||||
Qy    124 MAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRNKCQYCR 183

Db    130 fqkclalgmshnairfgrmpeaekrklvagltanegsqynpqvadlkafskhiynaylkn 189
          ||||||:|||||||||||||:||| ||:| ::::   | ||: |||:|::||:|::|:|:
Qy    184 FQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDID-QLNPESADLRALAKHLYDSYIKS 242

Db    190 fnmtkkkarsiltgkashtapfvihdietlwqaekglvwkqlvnglppykeisvhvfyrc 249
          | :|| |||:|||||::  :|||| |:::|  :|  :  |::       ||:::::|  |
Qy    243 FPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGC 302

Db    250 qcttvetvreltefaksipsfsslflndqvtllkygvheaifamlasivnkdgllvangs 309
          |  :||:|:|:||:|||||:| :| ||||||||||||||| |::||||::||||:|:::|
Qy    303 QFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQ 362

Db    310 gfvtreflrslrkpfsdiiepkfefavkfnalelddsdlalfiaaiilcgdrpglmnvpr 369
          ||:|||||:||||||:|::|||||||||||||||||||:||| ||| |||||||:||
Qy    363 GFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKP 422

Db    370 veaiqdtilralefhlqanhpdaqylfpkllqkmadlrqlvtehaqmmqrikktetetsl 429
          :| ||| :|:|||::|  |||::  ||:||||||:||||:|||| |::| ||||||: ||
Qy    423 IEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSL 482

Db    430 hpllqeiykdmy 441
          ||||||||||:|
Qy    483 HPLLQEIYKDLY 494
```

RESULT 2
ID R33745 standard; Protein; 439 AA.
AC R33745;
DT 23-JUL-1993 (first entry)
DE XR4.
KW Receptor; XR4; DNA binding domain; murine; glucocorticoid receptor;
KW hRAR-alpha; thyroid receptor-beta; retinoic acid receptor-alpha;
KW hGR; retinoid X receptor-alpha; hRXR-alpha; verht3; verhr5; ligand;
KW transcription-activation; response element; hTR-beta.
OS Mus musculus.
PN WO9306215-A.
PD 01-APR-1993.
PF 08-SEP-1992; U07570.
PR 17-SEP-1991; US-761068.
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
PI Borgmeyer UK, Evans RM, Giguere V, Mangelsdorf DJ;
PI Ong ES, Oro AE, Yao TP;
DR WPI; 93-117536/14.
DR N-PSDB; Q39089.
PT DNA encoding proteins of thyroid-steroid hormone receptor
PT super-family - useful for screening for agonists-antagonists of
PT such receptors
PS Claim 9; Page 44-46; 71pp; English.
CC This sequence represents the receptor XR4. This polypeptide has a
CC DNA binding domain comprising approx. 62% amino acid sequence identity
CC with the DNA binding domain of human retinoic acid receptor-alpha
CC (hRAR-alpha), about 58% amino acid sequence identity with the DNA
CC binding domain of human thyroid receptor-beta (hTR-beta), about 48%
CC amino acid sequence identity with the DNA binding domain of human
CC glucocorticoid receptor (hGR) and about 62% amino acid sequence
CC identity with the DNA binding domain of human retinoid X receptor-
CC alpha (hRXR-alpha). XR4 receptor can be used for testing a compound
CC for its ability to regulate transcription-activating effects of a



CC receptor polypeptide, identifying compounds which act as ligands for
CC the receptor polypeptides and for identifying response elements for
CC the receptor polypeptides.
SQ Sequence 439 AA;

DB 6; Score 1862; Match 62.3%; QryMatch 51.5%; Pred. No. 3.09e-141;
Matches 236; Conservative 89; Mismatches 52; Indels 2; Gaps 2;

```
Db     62 dgasggslnmecrvcgdkasgfhygvhacegckgffrrtirmkleyekcdrickiqkknr 121
          : :| : : :|||||||||||||||||||||||||||||||:|| |::||  |:|:||:|
Qy    117 EEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSR 176

Db    122 nkcqycrfqkclalgmshnairfgrmpdgekrklvagltasegcqhnpqladlkafskhi 181
          ||||||||||||:|||||||||||||::|| ||:| :::    | ||: |||:|::||:
Qy    177 NKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDID-QLNPESADLRALAKHL 235

Db    182 ynaylknfnmtkkkapsiltgksshnapfvihdietlwqaekglvwkqlvnvp-pyneis 240
          |::|:|:| :|| || :|||||:: ::|||| |:::|  :|  :  |::  :    :|::
Qy    236 YDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVA 295

Db    241 vhvfyrcqsttvetvreltefaknipnfsslflndevtllkygvheaifamlasivnkdg 300
          :::|  ||  :||:|:|:||:|||:|| | :| |||:|||||||||| |::||||::||||
Qy    296 IRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDG 355

Db    301 llvangsgfvtheflrslrkpfsdiiepkfefavkfnalelddtdlalfiaaiilcgdrp 360
          :|:::| ||:|:|||:|||||:|::|||||||||||||||||:|||:||| ||| ||||
Qy    356 VLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRP 415

Db    361 glmnvpqveaiqdtilralefhlqvnhpdsqylfpkllqkmadlrhvvtehaqmmqwlkk 420
          ||:||  :| ||| :|:|||::| :|||:|  ||:|||||:|||::|||| |::| :||
Qy    416 GLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKK 475

Db    421 tesqtllhpllqeiykdmy 439
          ||::  ||||||||||:|
Qy    476 TETDMSLHPLLQEIYKDLY 494
```

RESULT 3
ID R13791 standard; Protein; 1237 AA.
AC R13791;
DT 29-NOV-1991 (first entry)
DE E75A protein.
KW Insect steroid receptor; hormone.
OS Drosophila melanogaster.
FH Key Location/Qualifiers
FT Region 771
FT /note= "cDNA clone Dm4925 codes for Arg not Leu"
PN WO9113167-A.
PD 05-SEP-1991.
PF 15-FEB-1991; U01189.
PR 26-FEB-1990; US-485749.
PA (STRD ) LELAND STANFORD JR UNIV.
PI Hogness DS, Koelle MR, Segraves WA;
DR WPI; 91-281480/38.
DR N-PSDB; Q13572.
PT DNA encoding insect steroid receptors - and ligands, for use as
PT benign inducing factors
PS Disclosure; Page 94; 126pp; English.
CC The protein is encoded by the E75A transcription unit. The E75
CC proteins show considerable similarity to members of the steroid
CC receptor family. Since the putative hormone binding E domain of the
CC E75 proteins does not show high sequence homology to the known
CC ecdysone receptor (R13793) it is likely that the E75 proteins bind
CC either a terpenoid juvenile hormone or a novel Drosophila hormone.

```
CC   See also R13792-R13794.
SQ   Sequence   1237 AA;

  DB  3;  Score     680;  Match 33.3%;  QryMatch 18.8%;  Pred. No. 1.22e-43;
  Matches   120;  Conservative   93;  Mismatches 130;  Indels  17;  Gaps  15;

Db    242 tvlcpvcgdkasgfhygvhssegckgffrrsiqqkiqyrpctknqqcsilrinrnrcqyc 301
          :: | ||||||||||||||: ||||||||:|: |: |  |  :  | | : :||:|||
Qy    125 AIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRC--DLNCRIHKKSRNKCQYC 182

Db    302 rlkkciavamsrdavrfgrvpkrekarilaamqqst-q-nr-gqq-ralatel-ddqprl 356
          |: ||:||:|||::|:||||:|  || ::|| :     | |  : : ||||  | |   :
Qy    183 RFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKS 242

Db    357 la-avlrahletceftkekvs-amrqrardcpsysmptl-lacplnpapelqseqefsq- 412
          :: :  :|:      | :| :  : :      :  :  :    ||   :  : : |
Qy    243 FPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGC 302

Db    413 pfahv--irgvidfagmipgfqlltqddkftllkaglfdalfvrlicmfdssinsiicln 470
          |  |  :: : ::|  ||||  |  :|  |||| |: : ::  |  : :    :|  :
Qy    303 QFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKD-GVLIS-E 360

Db    471 gqv-mrrdaiqngana-gflvdstfnfaermnsmnltdaeiglfcaivlitpdrpglrnl 528
          ||  | |: : :  :: | :::: |:|| : |:::| |:::::| |::::: ||||| |:
Qy    361 GQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNV 420

Db    529 eliekmysrlkgclqyivaqnrpdqpeflaklletmpdlrtlstlhteklvvfrtehkel 588
            ||  :   |   |:  :  |:|: ::::|||||: | ||| : | | : | |::    ::
Qy    421 KPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDM 480


RESULT    4
ID   P80921 standard; protein; 456 AA.
AC   P80921;
DT   29-DEC-1990  (first entry)
DE   Sequence encoded by human placenta thyroid receptor c-erbA cDNA
KW   Hormone receptor; hormone-binding; transcription activation.
OS   Homo sapiens.
PN   WO8803168-A.
PD   05-MAY-1988.
PF   23-OCT-1987; U02782.
PR   20-OCT-1987; US-108471.
PA   (SALK) Salk Inst for Biol Stud.
PI   Evans RM, Weinberger CA, Hollenberg SM, Giguere V;
DR   WPI; 88-133242/19.
DR   N-PSDB; N80918.
PT   Recombinant DNA encoding hormone recpetors -
PT   comprising glucocorticoid, mineralocorticoid, thyroid hormone
PT   and novel hormone receptors
PS   Claim 17; Fig III-1(B)-1 and -2; 243pp; English.
CC   DNAs encoding hormone receptors and the hormone receptors themselves are
CC   claimed. The DNA can be used to make the hormone receptor proteins and
CC   functional modified forms in quantities not previously possible. The
CC   receptor proteins can be used to screen cpds. for receptor-agonist or
CC   receptor-antagonist activity. They can also be used in diagnostic assays.
SQ   Sequence   456 AA;

  DB  2;  Score     512;  Match 31.1%;  QryMatch 14.2%;  Pred. No. 3.89e-30;
  Matches   116;  Conservative  101;  Mismatches 130;  Indels  26;  Gaps  25;

Db    102 cvvcgdkatgyhyrcitcegckgffrrtiqknlhpsyskyegkcvidkvtrnqcqecrf 161
          | ||||||:|:||   :|||||||||||| : |   |  : : :| | | :|| || |||
Qy    128 CRVCGDKASGFHYGVHACEGCKGFFRRTI-R-LKLIYD-RCDLNCRIHKKSRNKCQYCRF 184
```



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Db    162 kkciyvgmatdlv-lddskrlakrkliee-nre-kr-rreelq-ksig-hkpeptdeewe 215
          ||: |||: : : :    :  | ||: | : :  :   |  : :::: |  ::
Qy    185 QKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFP 244

Db    216 liktlteahvatnaqg-shw-k-qkpkfl-ped-igqapivnapeggk-vdleaf-s-hf 267
          | |: : | :: ::   |     ::  ::  || |    |    | :| | :  | : :|
Qy    245 LTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQF 304

Db    268 tkiitpaitrvvdfakklpmfcelpcedqiillk-gccmeimslraavrydpesetltln 326
          : :  |:  : ::|| :| | :|  :||: ||| |    | :: |::  : ::  |  :
Qy    305 -RSVE-AVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLM-NKDG-VLISE 360

Db    327 gemavirgqlkn--gglgvvsdaifdlgmslssfnlddtevallqavllmssdrpglacv 384
          |:  : |  ||:    :|   :: |:::: :::::|||:::|:: ||:::|:|||||  |
Qy    361 GQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNV 420

Db    385 eriekyqdsfllafehyinyrkhhvthfwpkllmkvtdlrmigachasrflhmkvecpte 444
            ||  ||::| |:|  ::      ::: :||| |:|||| | : |  ::|::     |:
Qy    421 KPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHV-QLLQVIKKTETD 479

Db    445 l-lppiflevfed 456
          : | ||: |:: |
Qy    480 MSLHPLLQEIYKD 492


RESULT    5
ID   P80936 standard; protein; 410 AA.
AC   P80936;
DT   29-DEC-1990  (first entry)
DE   Sequence encode by thyroid hormone receptor cDNA from rat brain clone
DE   rbeA12
KW   Hormone receptor; hormone-binding; transcription activation.
OS   Rat.
PN   WO8803168-A.
PD   05-MAY-1988.
PF   23-OCT-1987; U02782.
PR   20-OCT-1987; US-108471.
PA   (SALK) Salk Inst for Biol Stud.
PI   Evans RM, Weinberger CA, Hollenberg SM, Giguere V;
DR   WPI; 88-133242/19.
DR   N-PSDB; N80923.
PT   Recombinant DNA encoding hormone recpetors -
PT   comprising glucocorticoid, mineralocorticoid, thyroid hormone
PT   and novel hormone receptors
PS   Example; Fig VII-1(B); 243pp; English.
CC   DNAs encoding hormone receptors and the hormone receptors themselves are
CC   claimed. The DNA can be used to make the hormone receptor proteins and
CC   functional modified forms in quantities not previously possible. The
CC   receptor proteins can be used to screen cpds. for receptor-agonist or
CC   receptor-antagonist activity. They can also be used in diagnostic assays.
SQ   Sequence   410 AA;

  DB  2;  Score     510;  Match 30.7%;  QryMatch 14.1%;  Pred. No. 5.61e-30;
  Matches   115;  Conservative   96;  Mismatches 137;  Indels  26;  Gaps  25;

Db     52 qcvvcgdkatgyhyrcitcegckgffrrtiqknlhptysckydsccvidkitrnqcqlcr 111
          :| ||||||:|:||   :|||||||||||| : |   |  : |  | | | :|| || ||
Qy    127 ECRVCGDKASGFHYGVHACEGCKGFFRRTI-R-LKLIYD-RCDLNCRIHKKSRNKCQYCR 183

Db    112 fkkciavgmamdlv-lddskrvakrklieq-nrerrr-k-eem-irslqqrp-eptpeew 165
          | ||:||||: : : :    :  | ||: : : :  : : |   :|:|  :  ::
Qy    184 FQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSF 243

Db    166 dlihv-ateahrstnaqgshw-k-qrrkfl-pdd-igqspivsmpdgdk-vdleaf-s-e 217
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Qy    244 PLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQ 303

Db    218 ftkiitpaitrvvdfakklpmfselpcedqiillk-gccmeimslraavrydpesdtltl 276

Qy    304 F-RSVE-AVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLM-NKDG-VLIS 359

Db    277 sqemtvkrkqlkn--gglgvvsdaifelgkslsafnlddtevallqavllmstdrsgllc 334

Qy    360 EGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLN 419

Db    335 vdkieksqeayllafehyvnhrkhniphfwpkllmkvtdlrmigachasrflhmkvecpt 394

Qy    420 VKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHV-QLLQVIKKTET 478

Db    395 el-fpplflevfed 407

Qy    479 DMSLHPLLQEIYKD 492
```

RESULT 6
ID R47621 standard; Protein; 514 AA.
AC R47621;
DT 07-JUL-1994 (first entry)
DE Rat thyroid hormone receptor.
KW Pituitary-specific thyroid hormone receptor; PSTHR; erbA gene;
KW hypothyroidism; hyperthyroidism.
OS Rattus sp.
PN US5284999-A.
PD 08-FEB-1994.
PF 05-APR-1990; 504806.
PR 05-APR-1990; US-504806.
PR 13-MAY-1993; US-069643.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PI Chin WW, Hodin RA, Lazar MA;
DR WPI; 94-056439/07.
DR P-PSDB; Q54086.
PT Recombinant DNA molecule encodes pituitary-specific thyroid
PT hormone receptor - useful for therapy of e.g. hypo- and
PT hyper-thyroidism
PS Disclosure; Column 21-22; 12pp; English.
CC A rat GH3 cell cDNA library was screened with rat erbA sequences to
CC isolate a gene encoding PSTHR. The sequence of the full-length cDNA
CC for PSTHR is given in Q54086, and the deduced amino acid sequence in
CC R47621.
SQ Sequence 514 AA;

DB 8; Score 501; Match 31.1%; QryMatch 13.9%; Pred. No. 2.92e-29;
Matches 116; Conservative 101; Mismatches 130; Indels 26; Gaps 25;

```
Db    160 cvvcgdkatgyhyrcitcegckgffrrtiqkslhpsysckyegkciidkvtrnqcqecrf 219

Qy    128 CRVCGDKASGFHYGVHACEGCKGFFRRTI-R-LKLIYD-RCDLNCRIHKKSRNKCQYCRF 184

Db    220 kkciyvgmatdlv-lddskrlakrkliee-nrq-kr-rreelq-ksig-hkpeptdeewe 273

Qy    185 QKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFP 244

Db    274 liktvteahvatnaqg-shw-k-qkrkfl-ped-igqapivnapeggk-vdleaf-s-hf 325

Qy    245 LTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQF 304

Db    326 tkiitpaitrvvdfakklpmfcelpcedqiillk-gccmeimslraavrydpdsetltln 384
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Qy    305 -RSVE-AVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLM-NKDG-VLISE 360

Db    385 gemavtrgqlkn--gglgvvsdaifdlgmslssfnlddtevallqavllmssdrrglacv 442

Qy    361 GQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNV 420

Db    443 eriekyqdsfllafehyinyrkhhvthfwpkllmkvtdlrmigachasrflhmkvecpte 502

Qy    421 KPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHV-QLLQVIKKTETD 479

Db    503 l-fpplflevfed 514

Qy    480 MSLHPLLQEIYKD 492
```

RESULT 7
ID R52980 standard; Protein; 461 AA.
AC R52980;
DT 06-OCT-1994 (first entry)
DE Human recombinant steroid hormone receptor NERI protein.
KW Steroid hormone receptor; NERI.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Binding_site 87..154
FT /note= "DNA binding area"
PN WO9407916-A.
PD 14-APR-1994.
PF 27-SEP-1993; U09165.
PR 07-OCT-1992; US-958137.
PA (MERI ) MERCK & CO INC.
PI Rodan GA, Rutledge SJ, Schmidt A, Vogel RL;
DR WPI; 94-135511/16.
DR N-PSDB; Q63134.
PT New human steroid receptor NERI and corresp. DNA - used to
PT develop assays to identify steroid hormone agonists and
PT antagonists
PS Claim 8; Page 31; 45pp; English.
CC The NERI protein may be expressed in a CHO cell culture and used
CC to develop assays to identify sterioid hormone agonists and
CC antagonists.
SQ Sequence 461 AA;

DB 9; Score 482; Match 29.8%; QryMatch 13.3%; Pred. No. 9.45e-28;
Matches 117; Conservative 91; Mismatches 161; Indels 23; Gaps 21;

```
Db     72 krkkgpapkmlghelcrvcgdkasgfhynvlscegckgffrrsvvrggarryacrgggtc 131

Qy    114 KPHEEPSNSLMAIE-CRVCGDKASGFHYGVHACEGCKGFFRRTI-RLKLI-YD-RCDLNC 169

Db    132 qmdafmrrkcqqcrlrkckeagmreqcvlseeqirkkkirkqqqqesqsqsqspvgpqgs 191

Qy    170 RIHKKSRNKCQYCRFQKCLAVGMSHN-AIRFG--RMPQAEKEKLLAEISSDIDQLNPESA 226

Db    192 sssasgpgaspggseagsqgsgegegvqltaaqelmiqqlvaaqlqcnkrsfsdqpkvtp 251

Qy    227 DLRALAKHLYDSYIKSFPLTKAKARAI-LTGKTTDK-SPFVIYDMNSLMMG-EDKIKFKH 283

Db    252 -wplgadpqsrdarqqrfahftel-aiisvqeivdfakqvpgflqlgredqiallkasti 309

Qy    284 ITPL-QE-QSKEVAIRIF-QGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVH 340

Db    310 eimlletarrynhetecitflkdftyskddfhra-glqv-efinpifefsramrrlgldd 367

Qy    341 EIIYTMLASLMNKDGVLISEGQGFM-TRE-FLKSLRKPFGDFMEPKFEFAVKFNALELDD 398
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```
Db    368 aeyalliainifsadrpnvqepgrvealqqpyveallsytrikrpqd-qlrfprmlmklv 426
          :: |::||: |:|:|:|| : :   :| :|:  ::||    ::::|:  || |:::| |:
Qy    399 SDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQL-FAKLLQKMT 457

Db    427 slrtlssvhse--qvfalrlqdkklppllsei 456
            || : : | :  ||:     |: | ||| ||
Qy    458 DLRQIVTEHVQLLQVIKKTETDMSLHPLLQEI 489


RESULT    8
ID   R27533 standard; Protein; 797 AA.
AC   R27533;
DT   09-MAR-1993  (first entry)
DE   myl/RAR-alpha fusion.
KW   Retinoic acid receptor; RAR-alpha; myl; acute promyelocytic leukemia;
KW   APL; translocation; chromosome 17; chromosome 15; PCR; primer;
KW   [t(15;17)(q21;q11-22)]; breakpoint; polymerase chain reaction.
OS   Synthetic.
PN   WO9216660-A.
PD   01-OCT-1992.
PF   23-MAR-1992; U02320.
PR   22-MAR-1991; US-673838.
PR   22-MAR-1991; US-675084.
PA   (SLOK ) SLOAN KETTERING INST CANCER.
PI   Dmitrovsky E, Evans RM, Frankel S, Kazizuka A, Miller WH;
PI   Warrell RP;
DR   WPI; 92-349240/42.
DR   N-PSDB; Q29334.
PT   Marker for acute promyelocytic leukaemia and other neoplasias -
PT   comprising nucleic acid and encoded abnormal retinoic acid
PT   receptor-alpha receptor
PS   Disclosure; Fig 4; 84pp; English.
CC   The sequence given shows a fusion between retinoic acid receptor
CC   (RAR)-alpha and myl which is characteristic of acute promyelocytic
CC   leukemia (APL).  This is caused by a translocation of a portion of
CC   the long arm of chromosome 17 onto the long arm of chromosome 15
CC   [t(15;17)(q21;q11-22)].  The breakpoint region has been cloned and it
CC   hsa been shown that DNA rearrangements are clustered in the region
CC   of the first intron of RAR-alpha.  This sequence was isolated by
CC   polymerase chain reaction (PCR) using primers which correspond to
CC   sequences both 5' and 3' to the breakpoint region.
SQ   Sequence   797 AA;

  DB  5;  Score     472;  Match 31.8%;  QryMatch 13.1%;  Pred. No. 5.87e-27;
  Matches   130;  Conservative  100;  Mismatches 137;  Indels  42;  Gaps  23;

Db    379 fkvrlqdlsscitqgkaietqsssseeivpsppspppl priykpcfvcqdkssgyhygvs 438
          : ::||:  | |    |     |  ::   |  |: : :   | || ||:||:||||
Qy     84 YDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVH 143

Db    439 acegckgffrrsiqknmvytchrdknciinkvtrnrcqycrlqkcfevgmskesvrndr- 497
          ||||||||||:|: :::|  : | || |:| :||:|||||:|||: |||| :::|  |
Qy    144 ACEGCKGFFRRTIRLKLIYD-RCDLNCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRM 202

Db    498 nkkkkevpkpe-csesytltpevgel--iek-vrkahqetfp---alcq--l-gk----- 542
            ||   :|  |:   | || ::|  : | :  :   :||   |  :  | ||
Qy    203 PQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKS 262

Db    543 -ytt-n-ns---seqrvsl-did-lwdkfselstk----c-i--iktv----efakqlpg 583
           :   : ||   :|::: :  | | :   |:: :    | :  : :|    |:|| :||
Qy    263 PFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPG 322

Db    584 fttltiadqitllkaacldililrictrytpeqdtmtfsdglt-lnrtqmhna--gfgpl 640
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          | | : ||:|||| :  :|:   : :    : | : :|:|   : |  : :    || :
Qy    323 FVNLDLNDQVTLLKYGVHEIIYTML-ASLM-NKDGVLISEGQGFMTREFLKSLRKPFGDF 380

Db    641 tdlvfafanqllplemddaetgllsaiclicgdrqdleqpdrvdmlqepllealkvyvrk 700
          :  | ||  : :||:||:: ::: |: :: |||  |     :: :|: ||:|| : ::
Qy    381 MEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKL 440

Db    701 rrpsrphmfpkmlmkitdlrsisakgaervitlkm-eipgsmppliqem 748
          :|  :::|:|:| |:|||| | :   : :  :|: |   |: ||:||:
Qy    441 NHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEI 489


RESULT    9
ID   R33744 standard; Protein; 440 AA.
AC   R33744;
DT   23-JUL-1993  (first entry)
DE   XR2.
KW   Receptor; XR2; DNA binding domain; human; retinoic acid receptor-alpha;
KW   hRAR-alpha; thyroid receptor-beta; hTR-beta; glucocorticoid receptor;
KW   hGR; retinoid X receptor-alpha; hRXR-alpha; verht3; verhr5; ligand;
KW   transcription-activation; response element.
OS   Homo sapiens.
PN   WO9306215-A.
PD   01-APR-1993.
PF   08-SEP-1992; U07570.
PR   17-SEP-1991; US-761068.
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
PI   Borgmeyer UK,  Evans RM,  Giguere V,  Mangelsdorf DJ;
PI   Ong ES,  Oro AE,  Yao TP;
DR   WPI; 93-117536/14.
DR   N-PSDB; Q39088.
PT   DNA encoding proteins of thyroid-steroid hormone receptor
PT   super-family - useful for screening for agonists-antagonists of
PT   such receptors
PS   Claim 9; Page 40-42; 71pp; English.
CC   This sequence represents the receptor XR2.  This polypeptide has a
CC   DNA binding domain comprising approx. 55% amino acid sequence identity
CC   with the DNA binding domain of human retinoic acid receptor-alpha
CC   (hRAR-alpha), about 56% amino acid sequence identity with the DNA
CC   binding domain of human thyroid receptor-beta (hTR-beta), about 50%
CC   amino acid sequence identity with the DNA binding domain of human
CC   glucocorticoid receptor (hGR) and about 52% amino acid sequence
CC   identity with the DNA binding domain of human retinoid X receptor-
CC   alpha (hRXR-alpha).  XR2 receptor can be used for testing a compound
CC   for its ability to regulate transcription-activating effects of a
CC   receptor polypeptide, identifying compounds which act as ligands for
CC   the receptor polypeptides and for identifying response elements for
CC   the receptor polypeptides.
SQ   Sequence   440 AA;

  DB  6;  Score     471;  Match 28.3%;  QryMatch 13.0%;  Pred. No. 7.05e-27;
  Matches   108;  Conservative  100;  Mismatches 147;  Indels  26;  Gaps  22;

Db     76 krkkgpapkmlgnelcsvcgdkasgfhynvlscdgckgffrrsvikgahyichsgghcpm 135
          |    |:  ::: | | |||||||||| | :|:|||||||::     |  :   :| :
Qy    114 KPHEEPSNSLMAIE-CRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYD-RCDLNCRI 171

Db    136 dtymrrkcqecplrkcrqaqmreecv----lse-eqirl-kklkrqeee-qahatsl-p- 186
          | ||| | ::||   ||  : :    ::: |  :|   :  : ::  : :: | :
Qy    172 HKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRAL 231

Db    187 prrssppqilp-qlspeql-gmi-eklva-aq-qqcnrrsfs-drlrvtpwpmap-dphs 239
          :::   : | :  |:     :::  |    :     :  |:     ::    ::| : :|
Qy    232 AKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQS 291
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Db    240 rearqqrfahftel-aivsvqeivdfakqlpgflqlsredqiallktsaievmlletsrr 298
          :|   : | :  :: :: :|||| ::|| :|||: |  :||::||| :  |::    :
Qy    292 KEVAIRIF-QGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASL 350

Db    299 ynpasesitflkdfsynredfaka-glqv-efinpifefsramnelqlndaefalliais 356
           |  :  |:    |   || | |:      :|::| |||:   | |:|:|:::|::||:
Qy    351 MNKDGVLISEGQGFM-TRE-FLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVI 408

Db    357 ifsadrpnvqdqlqverlqhtyvealhayvsihhphdrlmfprmlmklvslrtlssvhse 416
          |:|:||| : :   :| :|   ::||   : ::||    :|:::| |:  || : : | :
Qy    409 ILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQ 468

Db    417 --qvfalrlqdkklppllsei 435
            ||:     |: | ||| ||
Qy    469 LLQVIKKTETDMSLHPLLQEI 489


RESULT   10
ID   R27534 standard; Protein; 462 AA.
AC   R27534;
DT   09-MAR-1993  (first entry)
DE   RAR-alpha protein.
KW   Retinoic acid receptor; RAR-alpha; myl; acute promyelocytic leukemia;
KW   APL; translocation; chromosome 17; chromosome 15; PCR; primer;
KW   [t(15;17)(q21;q11-22)]; breakpoint; polymerase chain reaction.
OS   Synthetic.
PN   WO9216660-A.
PD   01-OCT-1992.
PF   23-MAR-1992; U02320.
PR   22-MAR-1991; US-673838.
PR   22-MAR-1991; US-675084.
PA   (SLOK ) SLOAN KETTERING INST CANCER.
PI   Dmitrovsky E, Evans RM, Frankel S, Kazizuka A, Miller WH;
PI   Warrell RP;
DR   WPI; 92-349240/42.
DR   N-PSDB; Q29338.
PT   Marker for acute promyelocytic leukaemia and other neoplasias -
PT   comprising nucleic acid and encoded abnormal retinoic acid
PT   receptor-alpha receptor
PS   Disclosure; Page 43-46; 84pp; English.
CC   The sequence given represents the amino acid sequence of the retinoic
CC   acid receptor (RAR)-alpha protein.  The gene encoding this protein is
CC   disrupted in a translocation of a portion of the long arm of chromosome
CC   17 onto the long arm of chromosome 15 [t(15;17)(q21;q11-22)].  This
CC   causes a fusion RAR-alpha and myl which is characteristic of acute
CC   promyelocytic leukemia (APL). The breakpoint region has been cloned
CC   and it has been shown that DNA rearrangements are clustered in the
CC   region of the first intron of RAR-alpha.  This sequence was isolated
CC   by polymerase chain reaction (PCR).  The primers used for amplification
CC   of this sequence can also be used to amplify the translocated region.
SQ   Sequence   462 AA;

  DB  5;  Score     464;  Match 33.4%;  QryMatch 12.8%;  Pred. No. 2.53e-26;
  Matches   122;  Conservative   91;  Mismatches 110;  Indels  42;  Gaps  23;

Db     88 cfvcqdkssgyhygvsacegckgffrrsiqknmvytchrdknciinkvtrnrcqycrlqk 147
          | || ||:||:|||| ||||||||||||:|: :::|  : | || |:| :|||:|||||:||
Qy    128 CRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYD-RCDLNCRIHKKSRNKCQYCRFQK 186

Db    148 cfevgmskesvrndr-nkkkkevpkpe-csesytltpevgel--iek-vrkahqetfp-- 200
          |: |||| :::|  |     ||   :|  |:   | || ::|  : | :  :   :||
Qy    187 CLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLT 246
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Db    201 -alcq--l-gk------ytt-n-ns---seqrvsl-did-lwdkfselstk----c-i-- 236
          `  |  :  | ||      :   : ||   :|::: :  |  | :   |:: :    | :
Qy    247 KAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRS 306

Db    237 iktv----efakqlpgfttltiadqitllkaacldililrictrytpeqdtmtfsdglt- 291
          : :|    |:|| :|||  | : ||:|||| :  :|:   : :    : | : :|:|
Qy    307 VEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTML-ASLM-NKDGVLISEGQGF 364

Db    292 lnrtqmhna--gfgpltdlvfafanqllplemddaetgllsaiclicgdrqdleqpdrvd 349
          : |  : :    || : :  | ||  : :||:||:: ::: |: :: |||  |     ::
Qy    365 MTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIE 424

Db    350 mlqepllealkvyvrkrrpsrphmfpkmlmkitdlrsisakgaervitlkm-eipgsmpp 408
           :|: ||:|| : ::  :|  :::|:|:| |:|||| | :   : :  :|: |   |: |
Qy    425 DIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHP 484

Db    409 liqem 413
          |:||:
Qy    485 LLQEI 489


RESULT   11
ID   R10547 standard; protein; 462 AA.
AC   R10547;
DT   11-APR-1991  (first entry)
DE   Murine Retinoic Acid Receptor-alpha (deduced from cDNA).
KW   mouse; retinoic acid receptor; mRAR-alpha; embryogenesis.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Region          1..59
FT   /label= Region A
FT   /note= "important for differential trans-activa-
FT   tion by other nuclear receptors"
FT   Region          60..87
FT   /label= Region B
FT   /note= "well conserved between mRAR's"
FT   Region          88..153
FT   /label= Region C
FT   /note= "DNA binding domain. 95 per cent amino acid
FT   identity between mRAR's"
FT   Region          154..199
FT   /label= Region D
FT   /note= "putative hinge region"
FT   Region          200..419
FT   /label= Region E
FT   /note= "ligand binding domain"
FT   Region          420..462
FT   /label= Region F
PN   EP-411323-A.
PD   06-FEB-1991.
PF   29-JUN-1990; 112469.
PR   30-JUN-1989; US-374690.
PR   29-MAR-1990; US-502140.
PA   (INRM ) INSERM INST NAT SANTE.
PA   (SQUI ) LES LABS SQUIBB SA.
PI   Chambon P, Kastner P, Krust A, Petkovich M, Zelent A;
PI   Leroy P, Mendelsoh C, Staub A;
DR   WPI; 91-038271/06.
PT   Novel human and mouse retinoic acid receptors - encode proteins
PT   used to assay for agonists and antagonists
PS   Disclosure; Fig 1; 33pp; English.
CC   An 11.5 day-old total mouse embryo lambda gt10 cDNA library was
CC   screened with labelled human RAR-alpha probes. Positive clones were
CC   isolated, mapped and sequenced. A set of mRAR-alpha clones was
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CC   identified on the basis of a 98 percent homology of their cDNA-
CC   deduced amino acid sequence with that of human RAR-alpha. There are
CC   8 amino acid substitutions (mostly conservative) between the human
CC   and mouse sequences. See also R10548, Q10388-9 and Q10405-8.
SQ   Sequence   462 AA;

  DB  2;  Score     463;  Match 33.4%;  QryMatch 12.8%;  Pred. No. 3.03e-26;
  Matches   122;  Conservative   91;  Mismatches 110;  Indels  42;  Gaps  23;

Db     88 cfvcqdkssgyhygvsacegckgffrrsiqknmvytchrdknciinkvtrnrcqycrlqk 147
           | || ||:||:|||| ||||||||||||:|: :::|  : | || |:| :||:|||||:|| 
Qy    128 CRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYD-RCDLNCRIHKKSRNKCQYCRFQK 186

Db    148 cfdvgmskesvrndr-nkkkkeapkpe-csesytltpevgel--iek-vrkahqetfp-- 200
           |: |||| :::|  |    ||   :|  |:   | || ::|  : | :  :   :||
Qy    187 CLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLT 246

Db    201 -alcq--l-gk------ytt-n-ns---seqrvsl-did-lwdkfselstk----c-i-- 236
           |  :  | ||      :   : ||   :|::: :  |  | :   |:: :    | :
Qy    247 KAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRS 306

Db    237 iktv----efakqlpgfttltiadqitllkaacldililrictrytpeqdtmtfsdglt- 291
           : :|    |:|| :|||  | : ||:|||| :  :|:   : :    : | : :|:|
Qy    307 VEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTML-ASLM-NKDGVLISEGQGF 364

Db    292 lnrtqmhna--gfgpltdlvfafanqllplemddaetgllsaiclicgdrqdleqpdkvd 349
           : |  : :    || : :  | ||  : :||:||:: ::: |: :: |||  |     ::
Qy    365 MTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIE 424

Db    350 mlqepllealkvyvrkrrpsrphmfpkmlmkitdlrsisakgaervitlkm-eipgsmpp 408
           :|: ||:|| : ::  :|  :::|:|:| |:|||| | :   : :  :|: |   |: |
Qy    425 DIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHP 484

Db    409 liqem 413
           |:||:
Qy    485 LLQEI 489


RESULT   12
ID   P90395 standard; protein;  462 AA.
AC   P90395;
DT   1-NOV-1989  (first entry)
DE   Retinoic acid receptor
KW   Clone phRAR1; retinoic acid receptor;
KW   ligand complexes; human.
OS   Homo sapiens (Human)
PN   WO8905355-A.
PD   15-JUN-1989.
PF   01-DEC-1988; U04284.
PR   02-DEC-1987; US-276536.
PA   (SALK) Salk Inst for Biological Stud.
PI   Evans RM, Giguere V, Ong ES, Segui PS, Umesono K, Thompson CC;
DR   WPI; 89-192701/26.
DR   N-PSDB; N90124.
PT   DNA encoding retinoic acid receptor proteins
PT   - used to produce proteins for studying complexes with
PT   ligands and in diagnostic assays.
PS   Disclosure; fig 1b; 74; English
CC   Primary sequence of a protein that has ligand binding and
CC   transcription activating properties of retinoic acid receptor
CC   (RAR) protein (see corresp. N90124).  Used to make chimeric
CC   receptors, to produce receptor, to study binding complexes,
CC   and to screen cpds. for RAR-agonists and antagonists.
SQ   Sequence   462 AA;
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  DB  1;  Score     462;  Match 33.4%;  QryMatch 12.8%;  Pred. No. 3.64e-26;
  Matches   122;  Conservative   91;  Mismatches 110;  Indels  42;  Gaps  23;

Db     88 cfvcqdkssgyhygvsacegckgffrrsiqknmvytchrdknciinkvtrnrcqycrlqk 147
           | || ||:||:|||| ||||||||||||:|: :::|  : | || |:| :||:|||||:|| 
Qy    128 CRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYD-RCDLNCRIHKKSRNKCQYCRFQK 186

Db    148 cfevgmskesvrndr-nkkkkevpkpe-csesytltpevgel--iek-vrkahqetfp-- 200
           |: |||| :::|  |    ||   :|  |:   | || ::|  : | :  :   :||
Qy    187 CLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLT 246

Db    201 -alcq--l-gk------ytt-n-ns---seqrvsl-did-lwdkfselstk----c-i-- 236
           |  :  | ||      :   : ||   :|::: :  |  | :   |:: :    | :
Qy    247 KAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRS 306

Db    237 iktv----efakqlpgfttltiadqitllkaacldililrictrytpeqdtmtfsdglt- 291
           : :|    |:|| :|||  | : ||:|||| :  :|:   : :    : | : :|:|
Qy    307 VEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTML-ASLM-NKDGVLISEGQGF 364

Db    292 lnrtqmhna--gfgpltdlvfafanqllplemddaetgllsaiclicgdrqdleqpdrvd 349
           : |  : :    || : :  | ||  : :||:||:: ::: |: :: |||  |     ::
Qy    365 MTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIE 424

Db    350 mlqepllealkvyvrkrrpsrphmfpkmlmkitdlrsisakgaervitlkm-eipgsmap 408
           :|: ||:|| : ::  :|  :::|:|:| |:|||| | :   : :  :|: |   |: |
Qy    425 DIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHP 484

Db    409 liqem 413
           |:||:
Qy    485 LLQEI 489


RESULT   13
ID   P90341 standard; protein;  448 AA.
AC   P90341;
DT   1-NOV-1989  (first entry)
DE   hap (hepatoma) protein
KW   hap protein; hepatoma protein; retinoic acid receptor; probe; human.
OS   Homo sapiens
PN   EP-321362-A.
PD   21-JUN-1989.
PF   16-DEC-1988; 403229.
PR   16-DEC-1987; US-278136.
PA   (INSP) Inst Pasteur.
PI   Tiollais P, Dejean A, Blaudin de The H, Marchio A;
DR   WPI; 89-180193/25.
DR   N-PSDB; N90093.
PT   New cloned hap gene
PT   - shows strong homology with retinoic acid receptor protein.
PS   Disclosure; fig 2; 46pp; English.
CC   Hap (hepatoma) protein (see corresp. N90093).  DNA isolated from
CC   human liver cDNA using a DNA fragment with a hepatitis B virus
CC   insert isolated from a hepatoma.  Specific hap fragments include
CC   amino acids 49-196, 151-167, 175-185, and 440-448.  The pure hap
CC   protein and its fragments can be used as probes for detn. and
CC   isolation of  complementary DNA and RNA sequences.  The hap
CC   protein shows strong homology with human retinoic acid receptor,
CC   RAR-beta, and can be used to assay for RAR (ant)agonists.
SQ   Sequence   448 AA;

  DB  1;  Score     459;  Match 32.9%;  QryMatch 12.7%;  Pred. No. 6.29e-26;
  Matches   120;  Conservative   91;  Mismatches 112;  Indels  42;  Gaps  24;
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Db     81 cfvcqdkssgyhygvsacegckgffrrsiqknmiytchrdkncvinkvtrnrcqycrlqk 140
          | || ||:||:|||| ||||||||||:|: ::||  : | || |:| :||:|||||:||
Qy    128 CRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYD-RCDLNCRIHKKSRNKCQYCRFQK 186

Db    141 cfevgmskesvrndr-nkkkketskqe-ctesyemtaelddl-t-ek-irkahqetfp-s 194
          |: |||| :::|  |     ||    | ::  :: :|  || :  | :  :   :|| :
Qy    187 CLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLT 246

Db    195 -l-cq--l-gk---------yttns--sadhrvrl-dlg-lwdkfselatk----c---- 228
              :  | ||         |  ||   :: ::::  :  | :   |:| :    |
Qy    247 KAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRS 306

Db    229 i--ik-ivefakrlpgftgltiadqitllkaacldililrictrytpeqdtmtfsdglt- 284
          :  :  | |:|| :|||  | : ||:|||| :  :|:   : :    : | : :|:|
Qy    307 VEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTML-ASLM-NKDGVLISEGQGF 364

Db    285 lnrtqmhna--gfgpltdlvftfanqllplemddtetgllsaiclicgdrqdleeptkvd 342
          : |  : :    || : :  | ||  : :||:||:: ::: |: :: |||  | :   ::
Qy    365 MTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIE 424

Db    343 klqepllealkiyirkrrpskphmfpkilmkitdlrsisakgaervitlkm-eipgsmpp 401
           :|: ||:|| : ::  :|  :::|:|:| |:|||| | :   : :  :|: |   |: |
Qy    425 DIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHP 484

Db    402 liqem 406
          |:||:
Qy    485 LLQEI 489
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RESULT   14
ID   R55128 standard; Protein; 448 AA.
AC   R55128;
DT   11-JAN-1995  (first entry)
DE   Retinoic acid receptor RAR-beta.
KW   Liver; hap; retinoic acid receptor; steroid; thyroid; hormone;
KW   hepatoma; retinoid; antibody.
OS   Homo sapiens.
PN   US5317090-A.
PD   31-MAY-1994.
PF   16-DEC-1987; 133687.
PR   16-DEC-1987; US-133687.
PR   17-DEC-1987; US-134130.
PR   20-JUN-1988; US-209009.
PR   30-NOV-1988; US-278136.
PR   30-MAR-1989; US-330405.
PR   21-AUG-1991; US-751612.
PR   30-MAR-1992; US-860577.
PR   11-DEC-1992; US-989902.
PA   (INSP ) INST PASTEUR.
PI   Brand N,  Chambon P,  De THE HB,  Dejean A,  Krust A;
PI   Marchio A, Petkovich M,  Tiollais P;
DR   WPI; 94-176333/21.
DR   N-PSDB; R55128.
PT   Antibody specific for retinoic acid receptor-beta - useful for
PT   detecting, quantifying and identifying agonists and antagonists
PT   of retinoid activity.
PS   Claim 1; Figure 2; 35pp; English.
CC   The retinoic acid receptor is encoded by a gene designated hap.  The
CC   hap gene is transcribed at low level in most human tissues, but the
CC   gene is overexpressed in prosate and kidney.  Six out of seven
CC   hepatoma or hepatoma-derived cell lines express a small hap
CC   transcript which is undetectable in normal adult and foetal livers
CC   but present in all non-hepatic tissues tested.
SQ   Sequence   448 AA;
```



```
  DB 10;  Score     457;  Match 32.9%;  QryMatch 12.6%;  Pred. No. 9.05e-26;
  Matches   120;  Conservative   92;  Mismatches 111;  Indels  42;  Gaps  24;

Db     81 cfvcqdkssgyhygvsacegckgffrrsiqknmiytchpdkncvinkvtrnrcqycrlqk 140
          | || ||:||:|||| ||||||||||:|: ::||  : | || |:| :||:|||||:||
Qy    128 CRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYD-RCDLNCRIHKKSRNKCQYCRFQK 186

Db    141 cfevgmskesvrndr-nkkkketskqe-ctesyemtaelddl-t-ek-irkahqetfp-s 194
          |: |||| :::|  |     ||    | ::  :: :|  || :  | :  :   :|| :
Qy    187 CLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLT 246

Db    195 -l-cq--l-gk---------yttns--sadhrvrl-dlg-lwdkfselatk----ciik- 231
              :  | ||         |  ||   :: ::::  :  | :   |:| :    | ::
Qy    247 KAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRS 306

Db    232 i--vq----fakrlpgftgltiadqitllkaacldililrictrytpeqdtmtfsdglt- 284
          :  ||    :|| :|||  | : ||:|||| :  :|:   : :    : | : :|:|
Qy    307 VEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTML-ASLM-NKDGVLISEGQGF 364

Db    285 lnrtqmhna--gfgpltdlvftfanqllplemddtetgllsaiclicgdrqdleeptkvd 342
          : |  : :    || : :  | ||  : :||:||:: ::: |: :: |||  | :   ::
Qy    365 MTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIE 424

Db    343 klqepllealkiyirkrrpskphmfpkilmkitdlrsisakgaervitlkm-eipgsmpp 401
           :|: ||:|| : ::  :|  :::|:|:| |:|||| | :   : :  :|: |   |: |
Qy    425 DIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHP 484

Db    402 liqem 406
          |:||:
Qy    485 LLQEI 489
```

```
RESULT   15
ID   R10548 standard; Protein; 448 AA.
AC   R10548;
DT   11-APR-1991  (first entry)
DE   Murine Retinoic Acid Receptor-beta (deduced from cDNA).
KW   mouse; retinoic acid receptor; mRAR-beta; embryogenesis.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Region          1..52
FT   /label= Region A
FT   /note= "important for trans-activation by other
FT   nuclear receptors"
FT   Region          53..80
FT   /label= Region B
FT   /note= "well conserved between mRAR's"
FT   Region          81..146
FT   /label= Region C
FT   /note= "DNA binding domain. 95 per cent amino
FT   acid identity between mRAR's"
FT   Region          147..192
FT   /label= Region D
FT   /note= "putative hinge region"
FT   Region          193..412
FT   /label= Region E
FT   /note= "ligand-binding domain"
FT   Region          413..448
FT   /label= Region F
PN   EP-411323-A.
PD   06-FEB-1991.
PF   29-JUN-1990; 112469.
PR   30-JUN-1989; US-374690.
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PR 29-MAR-1990; US-502140.
PA (INRM ) INSERM INST NAT SANTE.
PA (SQUI ) LES LABS SQUIBB SA.
PI Chambon P, Kastner P, Krust A, Petkovich M, Zelent A;
PI Leroy P, Mendelsoh C, Staub A;
DR WPI; 91-038271/06.
PT Novel human and mouse retinoic acid receptors - encode proteins
PT used to assay for agonists and antagonists
PS Disclosure; Fig 1; 33pp; English.
CC An 11.5 day-old total mouse embryo lambda gt10 cDNA library was
CC screened with labelled human RAR-beta probes. Positive clones were
CC isolated, mapped and sequenced. A set of mRAR-beta clones was
CC identified on the basis of a 98 percent homology of their cDNA-
CC deduced amino acid sequence with that of human RAR-beta. There are
CC 8 amino acid substitutions (mostly conservative) between the human
CC and mouse sequences. See also R10547, Q10388-9 and Q10405-8.
SQ Sequence 448 AA;

DB 2; Score 456; Match 32.9%; QryMatch 12.6%; Pred. No. 1.09e-25;
Matches 120; Conservative 91; Mismatches 112; Indels 42; Gaps 24;

```
Db     81 cfvcqdkssgyhygvsacegckgffrrsiqknmiytchrdkncvinkvtrnrcqycrlqk 140
          | || ||:||:|||| |||||||||||:|: ::||  : | || |:| :||:|||||:||
Qy    128 CRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYD-RCDLNCRIHKKSRNKCQYCRFQK 186

Db    141 cfevgmskesvrndr-nkkkkepskqe-ctesyemtaelddl-t-ek-irkahqetfp-s 194
          |: |||| :::|  |     ||    |  ::  :: :|  || :  | :  :   :|| :
Qy    187 CLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLT 246

Db    195 -l-cq--l-gk---------yttns--sadhrvrl-dlg-lwdkfselatk----c---- 228
             :  | ||         |  ||   :: ::::  :  | :   |:| :    |
Qy    247 KAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRS 306

Db    229 i--ik-ivefakrlpgftqltiadqitllkaacldililrictrytpeqdtmtfsdglt- 284
          :  :  | |:|| :|||  | : ||:|||| :  :|:   : :    : | : :|:|
Qy    307 VEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTML-ASLM-NKDGVLISEGQGF 364

Db    285 lnrtqmhna--gfgpltdlvftfanqllplemddtetgllsaiclcgdrqdleeptkvd 342
          : |  : :    || : :  | ||  : :||:||:: ::: |: :: |||  | :   ::
Qy    365 MTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIE 424

Db    343 klqepllealkiyirkrrpskphmfpkilmkitdlrsisakgaervitlkm-eipgsmpp 401
           :|: ||:|| : ::  :|  :::|:|:| |:|||| | :   : :  :|: |   |: |
Qy    425 DIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHP 484

Db    402 liqem 406
          |:||:
Qy    485 LLQEI 489
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